GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 30, 2003, 11:24:51 ; Search time 94 Seconds
(without alignments)
853.371 Million cell updates/sec

Title: US-09-748-739A-2
Perfect score: 3260
Sequence: 1 MDSKVTIICIRFLFWFLLLC.....MDWKNQFNDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3239	99.4	602	21	AAY44573	Human wild type Bu
2	3239	99.4	602	21	AAY49471	Human wild-type bu
3	3239	99.4	602	21	AAY59235	Human butyryl chol
4	3235	99.2	602	21	AAY44574	Human Butyrylcholi
5	3234	99.2	602	21	AAY49483	Human butyryl chol
6	3233	99.2	602	14	AAR37442	Full-length human
7	3232	99.1	602	21	AAY49473	Human butyryl chol
8	3232	99.1	602	21	AAY49474	Human butyryl chol
9	3232	99.1	602	21	AAY49475	Human butyryl chol
10	3231	99.1	602	21	AAY49472	Human butyryl chol
11	3231	99.1	602	21	AAY49476	Human butyryl chol
12	3230	99.1	602	21	AAY49477	Human butyryl chol
13	3228	99.0	602	21	AAY49478	Human butyryl chol
14	3228	99.0	602	21	AAY49484	Human butyryl chol
15	3227	99.0	602	21	AAY49485	Human butyryl chol
16	3227	99.0	602	21	AAY49486	Human butyryl chol
17	3227	99.0	602	21	AAY49488	Human butyryl chol
18	3226	99.0	602	21	AAY49487	Human butyryl chol
19	3225	98.9	602	21	AAY49482	Human butyryl chol
20	3224	98.9	602	21	AAY49481	Human butyryl chol
21	3223	98.9	602	21	AAY49479	Human butyryl chol
22	3223	98.9	602	21	AAY49480	Human butyryl chol
23	2698.5	82.8	635	7	AAP60097	Sequence of protei
24	2698.5	82.8	635	14	AAR41509	Full-length foetal
25	1786.5	54.8	575	19	AAW39078	Torpedo californic
26	1785.5	54.8	575	19	AAW39079	Torpedo californic
27	1699.5	52.1	614	21	AAY49494	Human acetylcholin
28	1699.5	52.1	614	21	AAY49495	Human acetylcholin
29	1699.5	52.1	614	23	AAU11234	Human acetylcholin
30	1698.5	52.1	614	16	AAR80726	Human acetylcholin
31	1698.5	52.1	614	21	AAY49489	Human wild-type ac
32	1698.5	52.1	614	23	AAU11231	Human acetylcholin
33	1698.5	52.1	614	23	AAU11232	Human acetylcholin
34	1698.5	52.1	614	23	AAU11233	Human acetylcholin
35	1698.5	52.1	620	23	AAU11235	Human acetylcholin
36	1695.5	52.0	614	21	AAY49491	Human acetylcholin
37	1690.5	51.9	614	21	AAY49490	Human acetylcholin
38	1686.5	51.7	614	21	AAY49492	Human acetylcholin
39	1686.5	51.7	614	21	AAY49493	Human acetylcholin
40	1683.5	51.6	583	21	AAG80773	AchE protein fragm
41	1659	50.9	613	11	AAR06989	Human acetylcholin
42	1646.5	50.5	584	21	AAG80772	AchE protein. Uni
43	1613.5	49.5	826	20	AAY30101	An acetylcholinest
44	1612.5	49.5	566	20	AAY30100	Amino acid sequenc
45	1579	48.4	600	19	AAW48797	Human acetylcholin

ALIGNMENTS

RESULT 1
AAY44573
ID AAY44573 standard; Protein; 602 AA.
XX
AC AAY44573;
XX
DT 04-APR-2000 (first entry)
XX
DE Human wild type Butyrylcholinesterase (BCHE) protein.
XX
KW Butyrylcholinesterase; BCHE allele; neurological disease; treatment;
KW therapy; allelic variant; BCHE-K; apoE4 allele; neurofibromatosis;
KW non-AD neurological disease; Alzheimer's disease; Huntington's disease;
KW depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
KW Parkinson's disease; multi-infarct dementia; human.
XX
OS Homo sapiens.
XX
PN WO9966072-A2.
XX
PD 23-DEC-1999.
XX
PF 16-JUN-1999; 99WO-IB01298.
XX
PR 16-JUN-1998; 98US-0089406.
XX
PA (NOVA-) NOVA MOLECULAR INC.
XX
PI Sevigny P, Wiebusch H, Schappert K;
XX
DR WPI; 2000-126550/11.
DR N-PSDB; AAZ49470.
XX

```
PT   Prediction of drug efficacy for treating neurological diseases like
PT   Alzheimer's disease, neurofibromatosis, Huntington's disease -
XX
PS   Example 1; Fig 3; 37pp; English.
XX
CC   The present sequence is the wild type human butyrylcholinesterase (BCHE)
CC   protein. Determining BCHE allele status of a patient helps predicting
CC   risk for neurological diseases, efficacy of therapy and determining
CC   treatment protocol. Presence of BCHE allelic variant, BCHE-K and
CC   apoE4 allele indicate patient's risk for having a neurological
CC   disease. This method enables treating Alzheimer's disease, depression,
CC   neurofibromatosis, Huntington's disease, amyotrophic lateral sclerosis,
CC   multiple sclerosis, stroke, Parkinson's disease, multi-infarct dementia
CC   and other non-AD neurological diseases.
XX
SQ   Sequence   602 AA;

  Query Match             99.4%;  Score 3239;  DB 21;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 3.5e-288;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 2
AAY49471
ID   AAY49471 standard; protein; 602 AA.
XX
AC   AAY49471;
XX
DT   27-MAR-2000  (first entry)

XX
DE   Human wild-type butyryl cholinesterase (BuChE).
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA.
XX
OS   Homo sapiens.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-0446100.
XX
PR   19-MAY-1995;   95US-0446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning -
XX
PS   Disclosure; Columns 3-4; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC   that comprises substituting a histidine residue for 1 or more amino
CC   acid(s) within 6 Angstrom of an active site serine. The method may be
CC   used for enhancing organophosphate detoxifying capabilities of esterases
CC   (either human AChE, human BuChE and/or human CaE). The modified esterases
CC   may then be used to treat agricultural workers poisoned with
CC   organophosphates through contact with chemical such as sheep dips. They
CC   may also be used to treat military personnel contaminated by chemical
CC   weaponry such as nerve agents. Additionally, the esterases may also be
CC   used to decontaminate ground and buildings and equipment used to store,
CC   or contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA.
XX
SQ   Sequence   602 AA;

  Query Match             99.4%;  Score 3239;  DB 21;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 3.5e-288;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
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Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
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Db    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
          ||
Db    601 GL 602
```

RESULT 3
AAY59235
ID AAY59235 standard; protein; 602 AA.
XX
AC AAY59235;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human butyryl cholinesterase (BuChE) mutant.
XX
KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6001625-A.
XX
PD 14-DEC-1999.
XX
PF 19-MAY-1995; 95US-0446100.
XX
PR 19-MAY-1995; 95US-0446100.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Broomfield CA, Lockridge O, Millard CB;
XX
DR WPI; 2000-096137/08.
XX
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning -
XX
PS Disclosure; Columns 99-102; 64pp; English.
XX
CC The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC that comprises substituting a histidine residue for 1 or more amino
CC acid(s) within 6 Angstrom of an active site serine. The method may be
CC used for enhancing organophosphate detoxifying capabilities of esterases
CC (either human AChE, human BuChE and/or human CaE). The modified esterases
CC may then be used to treat agricultural workers poisoned with
CC organophosphates through contact with chemical such as sheep dips. They
CC may also be used to treat military personnel contaminated by chemical
CC weaponry such as nerve agents. Additionally, the esterases may also be
CC used to decontaminate ground and buildings and equipment used to store,
CC or contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA.
XX
SQ Sequence 602 AA;

```
  Query Match             99.4%;  Score 3239;  DB 21;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 3.5e-288;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
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Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
          ||
Db    601 GL 602
```

RESULT 4
AAY44574
ID AAY44574 standard; Protein; 602 AA.
XX
AC AAY44574;
XX
DT 04-APR-2000 (first entry)
XX
DE Human Butyrylcholinesterase-K (BCHE-K) protein.
XX
KW Butyrylcholinesterase-K; BCHE-K; BCHE allele; neurological disease;
KW therapy; treatment; allelic variant; apoE4 allele; neurofibromatosis;
KW non-AD neurological disease; Alzheimer's disease; Huntington's disease;
KW depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
KW Parkinson's disease; multi-infarct dementia; human.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers

```
FT   Misc-difference 567
FT                   /note= "Wild type Ala replaced with Thr"
XX
PN   WO9966072-A2.
XX
PD   23-DEC-1999.
XX
PF   16-JUN-1999;   99WO-IB01298.
XX
PR   16-JUN-1998;   98US-0089406.
XX
PA   (NOVA-) NOVA MOLECULAR INC.
XX
PI   Sevigny P,  Wiebusch H,  Schappert K;
XX
DR   WPI; 2000-126550/11.
DR   N-PSDB; AAZ49471.
XX
PT   Prediction of drug efficacy for treating neurological diseases like
PT   Alzheimer's disease, neurofibromatosis, Huntington's disease -
XX
PS   Disclosure; Fig 4; 37pp; English.
XX
CC   The present sequence is the  human polymorphic variant
CC   butyrylcholinesterase-K (BCHE-K) protein. BCHE-K is an allelic variant
CC   of BCHE. Determining BCHE allele status (homozygous or heterozygous) of a
CC   patient helps predicting risk of neurological diseases, efficacy of
CC   therapy and determining treatment protocol. BCHE-K and apoE4 allele
CC   status also indicate patient's risk for having a neurological disease.
CC   This method enables treating Alzheimer's disease, Huntington's disease,
CC   depression, neurofibromatosis, amyotrophic lateral sclerosis, stroke,
CC   multiple sclerosis, Parkinson's disease, multi-infarct dementia and
CC   other non-AD neurological diseases.
XX
SQ   Sequence   602 AA;

  Query Match             99.2%;  Score 3235;  DB 21;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 8.1e-288;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDETEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 5
AAY49483
ID   AAY49483 standard; protein; 602 AA.
XX
AC   AAY49483;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human butyryl cholinesterase (BuChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-0446100.
XX
PR   19-MAY-1995;   95US-0446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning -
XX
PS   Disclosure; Columns 9-10; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC   that comprises substituting a histidine residue for 1 or more amino
CC   acid(s) within 6 Angstrom of an active site serine. The method may be
CC   used for enhancing organophosphate detoxifying capabilities of esterases
CC   (either human AChE, human BuChE and/or human CaE). The modified esterases
CC   may then be used to treat agricultural workers poisoned with
CC   organophosphates through contact with chemical such as sheep dips. They
CC   may also be used to treat military personnel contaminated by chemical
CC   weaponry such as nerve agents. Additionally, the esterases may  also be
CC   used to decontaminate ground and buildings and equipment used to store,
CC   or contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA.
XX
SQ   Sequence   602 AA;

  Query Match             99.2%;  Score 3234;  DB 21;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1e-287;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db      1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVLIWIYGGGFHTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
          ||
Db    601 GL 602
```

```
RESULT 6
AAR37442
ID   AAR37442 standard; Protein; 602 AA.
XX
AC   AAR37442;
XX
DT   06-OCT-1993  (first entry)
XX
DE   Full-length human pseudocholinesterase.
XX
KW   butylcholinesterase; acylcholine acylhydrolase; EC3.1.1.8; psi-ChE;
KW   pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;
KW   antidote.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /note= "putative leader peptide"
FT   Modified-site   45..47
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   134..136
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   269..271
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   284..286
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   369..371
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   509..511
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   514..516
FT                   /note= "potential N-glycosylation site"
FT   Active-site     226
FT                   /note= "active site Serine"
XX
PN   US5215909-A.
XX
PD   01-JUN-1993.
XX
PF   18-JUN-1986;   86US-0875737.
XX
PR   18-JUN-1986;   86US-0875737.
PR   21-AUG-1987;   87US-0087724.
PR   15-AUG-1990;   90US-0572911.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Soreq H;
XX
DR   WPI; 1993-188509/23.
DR   N-PSDB; AAQ42496.
XX
PT   Recombinant human gene encoding human pseudo-cholinesterase -
PT   used to treat organo-phosphorus poisoning
XX
PS   Disclosure; Columns 35-40; 34pp; English.
XX
CC   A cDNA library prepared from foetal brain mRNA was screened with
CC   degenerate probe pools based on the organophosphorus binding site of
CC   cholinesterases. A 764 nucleotide insert (designated FBChE12) was
CC   isolated from one positive clone and sequenced. This insert (AAQ42495),
CC   containing an ORF large enough to code for about half the subunit
CC   size of human cholinesterase, was used as a probe to obtain the full-
CC   length pseudocholinesterase sequence (AAQ42496).
XX
SQ   Sequence   602 AA;
```

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  Query Match             99.2%;  Score 3233;  DB 14;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-287;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLAWPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602
```

```
RESULT 7
AAY49473
ID   AAY49473 standard; protein; 602 AA.
XX
AC   AAY49473;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human butyryl cholinesterase (BuChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-0446100.
XX
PR   19-MAY-1995;   95US-0446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning -
XX
PS   Disclosure; Columns 3-4; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC   that comprises substituting a histidine residue for 1 or more amino
CC   acid(s) within 6 Angstrom of an active site serine. The method may be
CC   used for enhancing organophosphate detoxifying capabilities of esterases
CC   (either human AChE, human BuChE and/or human CaE). The modified esterases
CC   may then be used to treat agricultural workers poisoned with
CC   organophosphates through contact with chemical such as sheep dips. They
CC   may also be used to treat military personnel contaminated by chemical
CC   weaponry such as nerve agents. Additionally, the esterases may  also be
CC   used to decontaminate ground and buildings and equipment used to store,
CC   or contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA.
XX
SQ   Sequence   602 AA;
```

```
  Query Match           99.1%;  Score 3232;  DB 21;  Length 602;
  Best Local Similarity 99.5%;  Pred. No. 1.5e-287;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           ||||||||||||| ||||||||||||||||||||||||||||||||||||||||| ||||
Db     301 LLNEAFVVPYGTPHSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602
```

```
RESULT 8
AAY49474
ID   AAY49474 standard; protein; 602 AA.
XX
AC   AAY49474;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human butyryl cholinesterase (BuChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-0446100.
XX
PR   19-MAY-1995;   95US-0446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
```

```
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning -
XX
PS   Disclosure; Columns 3-6; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC   that comprises substituting a histidine residue for 1 or more amino
CC   acid(s) within 6 Angstrom of an active site serine. The method may be
CC   used for enhancing organophosphate detoxifying capabilities of esterases
CC   (either human AChE, human BuChE and/or human CaE). The modified esterases
CC   may then be used to treat agricultural workers poisoned with
CC   organophosphates through contact with chemical such as sheep dips. They
CC   may also be used to treat military personnel contaminated by chemical
CC   weaponry such as nerve agents. Additionally, the esterases may  also be
CC   used to decontaminate ground and buildings and equipment used to store,
CC   or contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA.
XX
SQ   Sequence   602 AA;

  Query Match            99.1%;  Score 3232;  DB 21;  Length 602;
  Best Local Similarity  99.5%;  Pred. No. 1.5e-287;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
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Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
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Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
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Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
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Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
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Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||
Db     301 LLNEAFVVPYGTPHSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
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Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
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Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 9
AAY49475
ID   AAY49475 standard; protein; 602 AA.
XX
AC   AAY49475;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human butyryl cholinesterase (BuChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-0446100.
XX
PR   19-MAY-1995;   95US-0446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning -
XX
PS   Disclosure; Columns 5-6; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC   that comprises substituting a histidine residue for 1 or more amino
CC   acid(s) within 6 Angstrom of an active site serine. The method may be
CC   used for enhancing organophosphate detoxifying capabilities of esterases
CC   (either human AChE, human BuChE and/or human CaE). The modified esterases
CC   may then be used to treat agricultural workers poisoned with
CC   organophosphates through contact with chemical such as sheep dips. They
CC   may also be used to treat military personnel contaminated by chemical
CC   weaponry such as nerve agents. Additionally, the esterases may  also be
CC   used to decontaminate ground and buildings and equipment used to store,
CC   or contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA.
XX
SQ   Sequence   602 AA;

  Query Match            99.1%;  Score 3232;  DB 21;  Length 602;
  Best Local Similarity  99.5%;  Pred. No. 1.5e-287;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
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Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
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Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
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Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
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Db    301 LLNEAFVVPYGTPLSHNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
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Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
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Qy    601 GL 602
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Db    601 GL 602
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RESULT 10
AAY49472
ID   AAY49472 standard; protein; 602 AA.
XX
AC   AAY49472;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human butyryl cholinesterase (BuChE) mutant G117H.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 145
FT                   /note= "wild-type Gly is replaced with His"
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-0446100.
XX
PR   19-MAY-1995;   95US-0446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning -
XX
PS   Claim 10; Columns 123-126; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)),
CC   that comprises substituting a histidine residue for 1 or more amino
CC   acid(s) within 6 Angstrom of an active site serine. The method may be
CC   used for enhancing organophosphate detoxifying capabilities of esterases
CC   (either human AChE, human BuChE and/or human CaE). The modified esterases
CC   may then be used to treat agricultural workers poisoned with
CC   organophosphates through contact with chemical such as sheep dips. They
CC   may also be used to treat military personnel contaminated by chemical
CC   weaponry such as nerve agents. Additionally, the esterases may  also be
CC   used to decontaminate ground and buildings and equipment used to store,
CC   or contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA.
XX
SQ   Sequence   602 AA;
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  Query Match             99.1%;  Score 3231;  DB 21;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.9e-287;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVLIWIYGGHFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          |||||||||||||| ||||||||||||||||||||||||||||||||||| ||||
Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
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Db    601 GL 602
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Search completed: January 30, 2003, 11:28:11
Job time : 96 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

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Title: US-09-748-739A-2
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Sequence: 1 MDSKVTIICIRFLFWFLLLC.....MDWKNQFNDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3239	99.4	602	3	US-08-446-100-1	Sequence 1, Appli
2	3239	99.4	602	3	US-08-446-100-24	Sequence 24, Appl
3	3239	99.4	602	4	US-09-334-489-3	Sequence 3, Appli
4	3235	99.2	602	4	US-09-334-489-4	Sequence 4, Appli
5	3234	99.2	602	3	US-08-446-100-13	Sequence 13, Appl
6	3233	99.2	602	6	5215909-11	Patent No. 5215909
7	3232	99.1	602	3	US-08-446-100-3	Sequence 3, Appli
8	3232	99.1	602	3	US-08-446-100-4	Sequence 4, Appli
9	3232	99.1	602	3	US-08-446-100-5	Sequence 5, Appli
10	3231	99.1	602	3	US-08-446-100-2	Sequence 2, Appli
11	3231	99.1	602	3	US-08-446-100-6	Sequence 6, Appli
12	3230	99.1	602	3	US-08-446-100-7	Sequence 7, Appli
13	3228	99.0	602	3	US-08-446-100-8	Sequence 8, Appli
14	3228	99.0	602	3	US-08-446-100-14	Sequence 14, Appl
15	3227	99.0	602	3	US-08-446-100-15	Sequence 15, Appl
16	3227	99.0	602	3	US-08-446-100-16	Sequence 16, Appl
17	3227	99.0	602	3	US-08-446-100-18	Sequence 18, Appl
18	3226	99.0	602	3	US-08-446-100-17	Sequence 17, Appl
19	3225	98.9	602	3	US-08-446-100-12	Sequence 12, Appl
20	3224	98.9	602	3	US-08-446-100-11	Sequence 11, Appl
21	3223	98.9	602	3	US-08-446-100-9	Sequence 9, Appli
22	3223	98.9	602	3	US-08-446-100-10	Sequence 10, Appl
23	2930	89.9	572	6	5200183-5	Patent No. 5200183
24	2698.5	82.8	635	6	5215909-10	Patent No. 5215909
25	2540.5	77.9	573	6	5215909-12	Patent No. 5215909
26	1786.5	54.8	575	1	US-08-348-920-1	Sequence 1, Appli
27	1783.5	54.7	575	1	US-08-348-920-2	Sequence 2, Appli
28	1699.5	52.1	614	3	US-08-446-100-25	Sequence 25, Appl
29	1698.5	52.1	614	1	US-07-732-962A-2	Sequence 2, Appli
30	1698.5	52.1	614	2	US-08-370-156-2	Sequence 2, Appli
31	1698.5	52.1	614	3	US-08-446-100-19	Sequence 19, Appl
32	1698.5	52.1	614	3	US-08-814-095-2	Sequence 2, Appli
33	1698.5	52.1	614	5	PCT-US92-06106-2	Sequence 2, Appli
34	1695.5	52.0	614	3	US-08-446-100-21	Sequence 21, Appl
35	1690.5	51.9	614	3	US-08-446-100-20	Sequence 20, Appl
36	1686.5	51.7	614	3	US-08-446-100-22	Sequence 22, Appl
37	1686.5	51.7	614	3	US-08-446-100-23	Sequence 23, Appl
38	1579	48.4	600	2	US-08-370-156-4	Sequence 4, Appli
39	1579	48.4	600	3	US-08-814-095-4	Sequence 4, Appli
40	1579	48.4	600	4	US-08-975-084-1	Sequence 1, Appli
41	1567	48.1	617	2	US-08-370-156-6	Sequence 6, Appli
42	1567	48.1	617	3	US-08-814-095-6	Sequence 6, Appli
43	1123	34.4	255	6	5215909-8	Patent No. 5215909
44	729	22.4	597	1	US-08-462-884A-1	Sequence 1, Appli
45	729	22.4	597	1	US-08-461-881B-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-1

  Query Match             99.4%;  Score 3239;  DB 3;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 3.7e-308;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
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Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
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Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
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Db     601 GL 602
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RESULT 2
US-08-446-100-24
; Sequence 24, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-24

  Query Match             99.4%;  Score 3239;  DB 3;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 3.7e-308;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
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Db     601 GL 602
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RESULT 3
US-09-334-489-3
; Sequence 3, Application US/09334489
; Patent No. 6291175
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; GENERAL INFORMATION:
;  APPLICANT:  Pierre Sevigny
;  APPLICANT:  Keith Schappert
;  APPLICANT:  Heiko Wiesbusch
;  TITLE OF INVENTION:  METHODS FOR TREATING A NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASE BY DETERMINING BCHE GENOTYPE
;  FILE REFERENCE:  08523/013002
;  CURRENT APPLICATION NUMBER: US/09/334,489
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  60/089,406
;  PRIOR FILING DATE:  1998-06-18
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-334-489-3

  Query Match             99.4%;  Score 3239;  DB 4;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 3.7e-308;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
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Db     601 GL 602


RESULT 4
US-09-334-489-4
; Sequence 4, Application US/09334489
; Patent No. 6291175
; GENERAL INFORMATION:
;  APPLICANT:  Pierre Sevigny
;  APPLICANT:  Keith Schappert
;  APPLICANT:  Heiko Wiesbusch
;  TITLE OF INVENTION:  METHODS FOR TREATING A NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASE BY DETERMINING BCHE GENOTYPE
;  FILE REFERENCE:  08523/013002
;  CURRENT APPLICATION NUMBER: US/09/334,489
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  60/089,406
;  PRIOR FILING DATE:  1998-06-18
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-334-489-4

  Query Match             99.2%;  Score 3235;  DB 4;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 9e-308;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
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Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
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Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
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Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
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Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
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Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDETEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
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Db     601 GL 602


RESULT 5
US-08-446-100-13
; Sequence 13, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
```

```
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-13

  Query Match             99.2%;  Score 3234;  DB 3;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.1e-307;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
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Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
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Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
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Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFHTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
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Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 6
5215909-11
;Patent No. 5215909
;    APPLICANT: SOREQ, HERMONA
;    TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
;    NUMBER OF SEQUENCES: 13
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/572,911
;      FILING DATE: 15-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 87,724
;      FILING DATE: 21-AUG-1987
;      APPLICATION NUMBER: 875,737
;      FILING DATE: 18-JUN-1986
;SEQ ID NO:11:
;      LENGTH: 602
5215909-11

  Query Match             99.2%;  Score 3233;  DB 6;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-307;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLAWPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
          ||
Db    601 GL 602


RESULT 7
US-08-446-100-3
; Sequence 3, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-3

  Query Match             99.1%;  Score 3232;  DB 3;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-307;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          |||||||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db    301 LLNEAFVVPYGTPHSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
          ||
Db    601 GL 602


RESULT 8
US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
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;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-4

  Query Match             99.1%;  Score 3232;  DB 3;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-307;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db     301 LLNEAFVVPYGTPHSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 9
US-08-446-100-5
; Sequence 5, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-5

  Query Match             99.1%;  Score 3232;  DB 3;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-307;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||| ||||||||||||||||||||||||||||||||||||| ||||
Db     301 LLNEAFVVPYGTPLSHNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
          ||
Db    601 GL 602


RESULT 10
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-2

  Query Match             99.1%;  Score 3231;  DB 3;  Length 602;
  Best Local Similarity   99.5%;  Pred. No. 2.2e-307;
  Matches  599;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVLIWIYGGHFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
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Db    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Db    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy    601 GL 602
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Db    601 GL 602


Search completed: January 30, 2003, 11:28:34
Job time : 17 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 30, 2003, 11:25:20 ; Search time 12 Seconds
(without alignments)
1012.291 Million cell updates/sec

Title: US-09-748-739A-2
Perfect score: 3260
Sequence: 1 MDSKVTIICIRFLFWFLLLC.....MDWKNQFNDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3260	100.0	602	10	US-09-748-739A-2	Sequence 2, Appli
2	3096	95.0	574	10	US-09-748-739A-17	Sequence 17, Appl
3	3092	94.8	574	10	US-09-748-739A-4	Sequence 4, Appli
4	3092	94.8	574	10	US-09-748-739A-20	Sequence 20, Appl
5	3089	94.8	574	10	US-09-748-739A-18	Sequence 18, Appl
6	3089	94.8	574	10	US-09-748-739A-19	Sequence 19, Appl
7	3088	94.7	574	10	US-09-748-739A-6	Sequence 6, Appli
8	3088	94.7	574	10	US-09-748-739A-8	Sequence 8, Appli
9	2774	85.1	574	10	US-09-748-739A-21	Sequence 21, Appl
10	2696	82.7	574	10	US-09-748-739A-22	Sequence 22, Appl
11	2505	76.8	574	10	US-09-748-739A-23	Sequence 23, Appl
12	1012	31.0	612	9	US-09-875-353-4	Sequence 4, Appli
13	973	29.8	574	9	US-10-023-515-4	Sequence 4, Appli
14	973	29.8	585	10	US-09-934-323-4	Sequence 4, Appli
15	879.5	27.0	816	9	US-09-875-353-2	Sequence 2, Appli
16	858.5	26.3	816	9	US-09-978-295A-375	Sequence 375, App
17	858.5	26.3	816	9	US-09-978-697-375	Sequence 375, App
18	858.5	26.3	816	9	US-09-978-192A-375	Sequence 375, App
19	858.5	26.3	816	9	US-09-999-832A-375	Sequence 375, App
20	858.5	26.3	816	9	US-09-978-189-375	Sequence 375, App
21	858	26.3	836	10	US-09-934-323-5	Sequence 5, Appli
22	853	26.2	835	10	US-09-934-323-2	Sequence 2, Appli
23	832	25.5	848	9	US-09-875-353-5	Sequence 5, Appli
24	752	23.1	581	9	US-10-023-515-2	Sequence 2, Appli
25	717	22.0	565	10	US-09-895-860-5	Sequence 5, Appli
26	700.5	21.5	583	10	US-09-925-301-1177	Sequence 1177, Ap
27	660.5	20.3	571	9	US-10-036-041-23	Sequence 23, Appl
28	660.5	20.3	571	9	US-10-028-072-542	Sequence 542, App
29	660.5	20.3	571	9	US-10-035-855-23	Sequence 23, Appl
30	660.5	20.3	571	12	US-10-036-342-23	Sequence 23, Appl
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32	656.5	20.1	554	10	US-09-895-860-4	Sequence 4, Appli
33	604	18.5	516	10	US-09-731-393-17	Sequence 17, Appl
34	603	18.5	529	10	US-09-731-393-12	Sequence 12, Appl
35	530	16.3	545	9	US-09-978-295A-254	Sequence 254, App
36	530	16.3	545	9	US-09-978-697-254	Sequence 254, App
37	530	16.3	545	9	US-09-978-192A-254	Sequence 254, App
38	530	16.3	545	9	US-09-999-832A-254	Sequence 254, App
39	530	16.3	545	9	US-09-978-189-254	Sequence 254, App
40	530	16.3	545	9	US-10-174-590-58	Sequence 58, Appl
41	530	16.3	545	9	US-10-176-758-58	Sequence 58, Appl
42	530	16.3	545	9	US-10-175-737-58	Sequence 58, Appl
43	530	16.3	545	12	US-10-052-586-58	Sequence 58, Appl
44	515.5	15.8	527	10	US-09-731-393-10	Sequence 10, Appl
45	507	15.6	525	10	US-09-731-393-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-748-739A-2
; Sequence 2, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-2

Query Match 100.0%; Score 3260; DB 10; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.9e-285;
Matches 602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
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Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
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Db     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
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Db    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
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Db    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
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Db    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
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Qy    601 GL 602
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Db    601 GL 602
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RESULT 2
US-09-748-739A-17
; Sequence 17, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-17

Query Match 95.0%; Score 3096; DB 10; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.6e-270;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 60

Qy     89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
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Db     61 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 120

Qy    149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
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Qy    209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
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Db    181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

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Db    301 DMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360

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Db    361 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 420

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Db    541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574
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RESULT 3
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Butyrylcholinesterase Variants and
; TITLE OF INVENTION: Methods of Use.
; FILE REFERENCE: P-IX 4143
; CURRENT APPLICATION NUMBER: US/09/748,739A
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-4

Query Match 94.8%; Score 3092; DB 10; Length 574;
Best Local Similarity 99.7%; Pred. No. 3.6e-270;
Matches 572; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
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Db    121 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy    209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy    269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
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Qy    329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
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Qy    509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
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Db    481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 540

Qy    569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
          |||||||||||||||||||||||||||||||||
Db    541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574


RESULT 4
US-09-748-739A-20
; Sequence 20, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-20

  Query Match             94.8%;  Score 3092;  DB 10;  Length 574;
  Best Local Similarity   99.7%;  Pred. No. 3.6e-270;
  Matches  572;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
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Qy     89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
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Db     61 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 120

Qy    149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
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Db    121 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy    209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
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Db    181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy    269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
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Qy    329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
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Db    301 DMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360

Qy    389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
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Qy    449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
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Db    421 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 480

Qy    509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDETE 540

Qy    569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
          |||||||||||||||||||||||||||||||||
Db    541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574


RESULT 5
US-09-748-739A-18
; Sequence 18, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-18

  Query Match             94.8%;  Score 3089;  DB 10;  Length 574;
  Best Local Similarity   99.7%;  Pred. No. 6.7e-270;
  Matches  572;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 60

Qy     89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YANSCCQNIGQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 120

Qy    149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy    209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy    269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

Qy    329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    301 DMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360

Qy    389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 420

Qy    449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 480

Qy    509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 540

Qy    569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
          |||||||||||||||||||||||||||||||||
Db    541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574


RESULT 6
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US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-19

  Query Match             94.8%;  Score 3089;  DB 10;  Length 574;
  Best Local Similarity   99.7%;  Pred. No. 6.7e-270;
  Matches  572;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 60

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 120

Qy     149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy     209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy     269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

Qy     329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     301 DMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360

Qy     389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 420

Qy     449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 480

Qy     509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     481 NETQNNSTSWPVFKSTVQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 540

Qy     569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           |||||||||||||||||||||||||||||||||||
Db     541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574


RESULT 7
US-09-748-739A-6
; Sequence 6, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-6

  Query Match             94.7%;  Score 3088;  DB 10;  Length 574;
  Best Local Similarity   99.7%;  Pred. No. 8.3e-270;
  Matches  572;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 60

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 120

Qy     149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy     209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy     269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTQLSVNFGPTVDGDFLT 300

Qy     329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     301 DMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360

Qy     389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 420

Qy     449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 480

Qy     509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 540

Qy     569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           |||||||||||||||||||||||||||||||||||
Db     541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574


RESULT 8
US-09-748-739A-8
; Sequence 8, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
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;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

  Query Match             94.7%;  Score 3088;  DB 10;  Length 574;
  Best Local Similarity   99.7%;  Pred. No. 8.3e-270;
  Matches  572;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
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Db       1 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 60

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 120

Qy     149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

Qy     209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy     269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTSLSVNFGPTVDGDFLT 300

Qy     329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 DMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 360

Qy     389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 420

Qy     449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 480

Qy     509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 540

Qy     569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           |||||||||||||||||||||||||||||||||
Db     541 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 574


RESULT 9
US-09-748-739A-21
; Sequence 21, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Equus caballus
US-09-748-739A-21

  Query Match             85.1%;  Score 2774;  DB 10;  Length 574;
  Best Local Similarity   90.5%;  Pred. No. 1.5e-241;
  Matches  517;  Conservative   20;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
           |:|||| |||||||||| | ||||||||||||||||||||||||||||||:||||||
Db       1 EEDIIITTKNGKVRGMNLPVLGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSNIWNATK 60

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
           ||||| || ||||||| |||||||:||||||||||||||||||:||||||||||
Db      61 YANSCYQNTDQSFPGFLGSEMWNPNTELSEDCLYLNVWIPAPKPKNATVMIWIYGGGFQT 120

Qy     149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
           ||||| |||||||||||||||||||||||||| | |||||||||| ||||||||||||||
Db     121 GTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLALSENPEAPGNMGLFDQQLALQWVQK 180

Qy     209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSSNAPWAVTSLYEAR 268
           |||||||||:|||||||||||||||||| | |||||||||| ||||||||||||||||||
Db     181 NIAAFGGNPRSVTLFGESAGAASVSLHLLSPRSQPLFTRAILQSGSSNAPWAVTSLYEAR 240

Qy     269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
           |||| |||  ||||:||||:|||||:|||||||||| ||||| | ||||||||||||||||
Db     241 NRTLTLAKRMGCSRDNETEMIKCLRDKDPQEILLNEVFVVPYDTLLSVNFGPTVDGDFLT 300

Qy     329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
           |||| ||:|||||:|||||||||| ||||||||||||||||||||||||||||||||||||
Db     301 DMPDTLLQLGQFKRTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPR 360

Qy     389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
           |||||:||||||| ||:|||| ||||||| ||||||| ||||||||:|||| ||:|||||
Db     361 VSEFGRESILFHYMDWLDDQRAENYREALDDVVGDYNIICPALEFTRKFSELGNDAFFYY 420

Qy     449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
           |||||:|||||||||||||||||||||||||| |||:||||||||:||||||||||||||
Db     421 FEHRSTKLPWPEWMGVMHGYEIEFVFGLPLERRVNYTRAEEILSRSIMKRWANFAKYGNP 480

Qy     509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
           | |||||| |||||||||||||| :: |||||||||||| ||||||||:||||||||
Db     481 NGTQNNSTRWPVFKSTEQKYLTLNTESPKVYTKLRAQQCRFWTLFFPKVLELTGNIDEAE 540

Qy     569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599
           |||||||||||||||||||||||||||||||
Db     541 REWKAGFHRWNNYMMDWKNQFNDYTSKKESC 571


RESULT 10
US-09-748-739A-22
; Sequence 22, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-748-739A-22

  Query Match             82.7%;  Score 2696;  DB 10;  Length 574;
  Best Local Similarity   87.6%;  Pred. No. 1.6e-234;
  Matches  503;  Conservative   22;  Mismatches   49;  Indels    0;  Gaps    0;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
           |:|||| |||||||||| | ||||||||||||||||||||||||||||||||||||||
Db       1 EEDIIITTKNGKVRGMNLPVLDGTVTAFLGIPYAQPPLGRLRFKKPQFLTKWSDIWNATK 60

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
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Db      61 YANSCYQNADQSFPGFPGSEMWNPNTDLSEDCLYLNVWIPTPKPKNATVMIWIYGGGFQT 120

Qy     149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208

Db     121 GTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEVPGNMGLFDQQLALQWVQK 180

Qy     209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268

Db     181 NIAAFGGNPKSVTLFGESAGAGSVSLHLLSPRSQPLFTRAILQSGSSNAPWAVMSLDEAK 240

Qy     269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328

Db     241 NRTLTLAKFIGCSKENDTEIIKCLRNKDPQEILLNELLVVPSDTLLSVNFGPVVDGDFLT 300

Qy     329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388

Db     301 DMPDTLLQLGQFKKTQILVGVNKDEGTAFLVYGAPGFSKDNDSIITRKEFQEGLKIYFPG 360

Qy     389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448

Db     361 VSEFGREAILFYYVDLLDDQRAEKYREALDDVLGDYNIICPALEFTTKFSELGNNAFFYY 420

Qy     449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508

Db     421 FEHRSSQLPWPEWMGVMHGYEIEFVFGLPLERRVNYTRAEEILSRSIMNYWANFAKYGNP 480

Qy     509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568

Db     481 NGTQNNSTRWPAFRSTDQKYLTLNAESPKVYTKLRAQQCRFWTLFFPKVLEMTGNIDEAE 540

Qy     569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602

Db     541 REWRAGFYRWNNYMMDWKNQFNDYTSKKESCAGL 574


Search completed: January 30, 2003, 11:28:53
Job time : 14 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 30, 2003, 11:24:50 ; Search time 22 Seconds
(without alignments)
2630.587 Million cell updates/sec

Title: US-09-748-739A-2
Perfect score: 3260
Sequence: 1 MDSKVTIICIRFLFWFLLLC.....MDWKNQFNDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3239	99.4	602	1	ACHU	cholinesterase (EC
2	2855.5	87.6	581	2	C39768	cholinesterase (EC
3	2593	79.5	603	2	S70849	cholinesterase (EC
4	1791.5	55.0	596	1	ACRYE	acetylcholinestera
5	1789.5	54.9	599	1	A38868	acetylcholinestera
6	1698.5	52.1	614	2	A39256	acetylcholinestera
7	1693.5	51.9	614	2	JH0811	acetylcholinestera
8	1692.5	51.9	614	2	JH0314	acetylcholinestera
9	1639	50.3	584	2	S48724	acetylcholinestera
10	1636.5	50.2	583	2	S10712	acetylcholinestera
11	1466	45.0	767	2	S47639	acetylcholinestera
12	1142	35.0	620	2	A54413	acetylcholinestera
13	1075.5	33.0	637	2	S66236	acetylcholinestera
14	1045	32.1	691	2	JE0150	acetylcholinestera
15	1044	32.0	746	2	A25363	acetylcholinestera
16	1025.5	31.5	602	2	T37254	acetylcholinestera
17	951	29.2	629	2	T37255	acetylcholinestera
18	937	28.7	584	2	T27009	hypothetical prote
19	930	28.5	607	2	T42399	acetylcholinestera
20	893	27.4	532	2	T33842	hypothetical prote
21	754	23.1	532	2	A34329	60K esterase (EC 3
22	753	23.1	141	2	G39768	cholinesterase (EC
23	740.5	22.7	559	1	JC5408	carboxylesterase (
24	733	22.5	599	2	A57701	sterol esterase (E
25	731.5	22.4	561	2	S47655	carboxylesterase (
26	729	22.4	597	2	A33668	sterol esterase (E
27	727	22.3	612	2	A34967	sterol esterase (E
28	724.5	22.2	554	2	A39060	carboxylesterase (
29	724	22.2	141	2	D39768	cholinesterase (EC
30	721	22.1	141	2	B39768	cholinesterase (EC
31	721	22.1	141	2	F39768	cholinesterase (EC
32	716	22.0	565	2	S10367	carboxylesterase (
33	713.5	21.9	562	2	A55281	carboxylesterase (
34	711	21.8	745	2	S13586	triacylglycerol li
35	707	21.7	141	2	E39768	cholinesterase (EC
36	701.5	21.5	557	2	A47162	thiolesterase B (E
37	700.5	21.5	567	1	A41010	carboxylesterase (
38	700	21.5	561	2	JC2447	carboxylesterase (
39	699.5	21.5	549	2	JX0054	carboxylesterase (
40	697	21.4	540	2	A31584	carboxylesterase (
41	692	21.2	561	2	S62788	carboxylesterase (
42	691	21.2	561	2	S71597	carboxylesterase (
43	690.5	21.2	566	2	S19307	carboxylesterase (
44	666	20.4	956	2	A56920	gliotactin precurs
45	656.5	20.1	554	1	S34607	carboxylesterase (

ALIGNMENTS

RESULT 1
ACHU
cholinesterase (EC 3.1.1.8) precursor [validated] - human
N;Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 08-Dec-2000
C;Accession: A33769; A26613; A33887; A34668; A00772
R;Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single
A;Reference number: A33769; MUID:90212557; PMID:2322535
A;Accession: A33769
A;Molecule type: DNA
A;Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLCHLCCRESEIN',1-602 <ARP>
A;Cross-references: GB:M32391; GB:J02879
A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for
R;Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A;Title: Isolation and characterization of full-length cDNA clones coding for choline
A;Reference number: A26613; MUID:87231856; PMID:3035536
A;Accession: A26613
A;Molecule type: mRNA
A;Residues: 1-133,'D',135-602 <PRO>
R;McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; R
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A;Title: Brain cDNA clone for human cholinesterase.
A;Reference number: A33887; MUID:88016155; PMID:3477799
A;Accession: A33887
A;Molecule type: mRNA
A;Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLYHLCCRESEIN',1-602 <MCT>
A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for
R;Nogueira, C.P.; McGuire, M.C.; Graeser, C.; Bartels, C.F.; Arpagaus, M.; Van der Sp
Am. J. Hum. Genet. 46, 934-942, 1990
A;Title: Identification of a frameshift mutation responsible for the silent phenotype
A;Reference number: A34668; MUID:90252779; PMID:2339692
A;Accession: A34668
A;Molecule type: DNA
A;Residues: 143-145,'VSNWNIIFTCL' <NOG>
A;Note: frameshift mutant in codon for residue 145 (Gly)
R;Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L
J. Biol. Chem. 262, 549-557, 1987
A;Title: Complete amino acid sequence of human serum cholinesterase.
A;Reference number: A00772; MUID:87109144; PMID:3542989
A;Accession: A00772
A;Molecule type: protein
A;Residues: 29-602 <LOC>
A;Experimental source: plasma
C;Comment: Cholinesterase is present in most cells (except erythrocytes).
C;Genetics:
A;Gene: GDB:BCHE; CHE1
A;Cross-references: GDB:120558; OMIM:177400
A;Map position: 3q26.1-3q26.2

```
A;Introns: 506/2; 562/1
C;Function:
A;Description: hydrolyzes acylcholines to choline and a carboxylic acid
A;Note: this cholinesterase is highly reactive with organophosphate esters
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-602/Product: cholinesterase #status experimental <MAT>
F;56-556/Domain: cholinesterase homology <CHE>
F;45,85,134,269,284,369,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status
F;226/Active site: Ser #status experimental

  Query Match             99.4%;  Score 3239;  DB 1;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 5.9e-238;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 2
C39768
cholinesterase (EC 3.1.1.8) - rabbit
N;Alternate names: butyrylcholinesterase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 20-Jun-2000
C;Accession: S10255; C39768
R;Jbilo, O.; Chatonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A;Title: Complete sequence of rabbit butyrylcholinesterase.
A;Reference number: S10255; MUID:90326526; PMID:2374720
A;Accession: S10255
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-581 <JBI>
A;Cross-references: EMBL:X52090; NID:g1476; PIDN:CAA36308.1; PID:g1370277
R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.
J. Biol. Chem. 266, 6966-6974, 1991
A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholir
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: C39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 75-215 <ARP>
A;Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789
C;Genetics:
A;Introns: 485/2; 541/1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;35-535/Domain: cholinesterase homology <CHE>

  Query Match             87.6%;  Score 2855.5;  DB 2;  Length 581;
  Best Local Similarity   91.4%;  Pred. No. 7.6e-209;
  Matches  531;  Conservative   12;  Mismatches   37;  Indels    1;  Gaps    1;

Qy      21 MLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKW 80
           |:   |||| |:|| ||||::||:|| ||||||||||||||||||||||||||||||||
Db       1 MVTRSSHTE-DVIITTKNGRIRGINLPVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKW 59

Qy      81 SDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIW 140
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||:||
Db      60 SDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPTPKPKNATVMIW 119

Qy     141 IYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQ 200
           |||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||
Db     120 IYGGGFQTGTSSLQVYDGKFLTRVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQ 179

Qy     201 LALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWA 260
           |||||||||||||||||||||||||||||||||||| || |||||||||| ||||
Db     180 LALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPRSHPLFTRAILQSGSSNAPWE 239

Qy     261 VTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGP 320
           | ||:||||||| ||| ||| |||||||||||||| ||||||| |||| : ||||.|||
Db     240 VMSLHEARNRTLTLAKFVGCSTENETEIIKCLRNKDAQEILLNEVFVVPFDSLLSVNFGP 299

Qy     321 TVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQE 380
           |||||||||||| ||:||| |||||||||||||| |||||||||||| ||||||||||
Db     300 TVDGDFLTDMPDTLLQLGQLKKTQILVGVNKDEGTAFLVYGAPGFSKDNTSIITRKEFQE 359

Qy     381 GLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEW 440
           |||||||||||||||||||||||||:|||||||||| ||||||||||||||||||||||
Db     360 GLKIFFPGVSEFGKESILFHYTDWVDEQRPENYREALDDVVGDYNFICPALEFTKKFSEW 419

Qy     441 GNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWA 500
           |||||||||||||||||||||||||||||||||||||||||| |||||||||||:||||
Db     420 GNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRVNYTKAEEILSRSIMKRWA 479

Qy     501 NFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEM 560
           ||||||||| |||||| |||||||||||||||||| || |||||||||||| ||||||||
Db     480 NFAKYGNPNGTQNNSTRWPVFKSTEQKYLTLNTESPRIYTKLRAQQCRFWTLFFPKVLEM 539

Qy     561 TGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVG 601
           ||||||||| ||||||||||||||| ||| |||||||||| | |
Db     540 TGNIDEAEQEWKAGFHRWNNYMMAWKNHFNDYTSKKERCAG 580


RESULT 3
S70849
cholinesterase (EC 3.1.1.8) - mouse
N;Alternate names: butyrylcholine esterase
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
C;Accession: S70849; S15680; A39768
R;Taylor, P.
submitted to the EMBL Data Library, August 1992
```

A;Reference number: S70849
A;Accession: S70849
A;Molecule type: nucleic acid
A;Residues: 1-603 <TAY>
A;Cross-references: EMBL:M99492; NID:g191579; PIDN:AAA37328.1; PID:g191580
R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
A;Reference number: JH0314; MUID:90380429; PMID:2400605
A;Accession: S15680
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 30-128,'P',130-603 <RAC>
A;Cross-references: EMBL:M99492
R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Noo
J. Biol. Chem. 266, 6966-6974, 1991
A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: A39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 97-128,'P',130-237 <ARP>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;57-557/Domain: cholinesterase homology <CHE>

Query Match 79.5%; Score 2593; DB 2; Length 603;
Best Local Similarity 80.4%; Pred. No. 7e-189;
Matches 475; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

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Qy      12 FLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRF 71
           || | ||||  ||||||:| || || |:|||::: | ||||||||||||||||| |||
Db      13 FLLWILLLCMPFGKSHTEEDFIITTKTGRVRGLSMPVLGGTVTAFLGIPYAQPPLGSLRF 72

Qy      72 KKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPK 131
           |||| | || || |||:|||| ||||:|||| |||||||||:|||||||||||  ||
Db      73 KKPQPLNKWPDIHNATQYANSCYQNIDQAFPGFQGSEMWNPNTNLSEDCLYLNVWIRVPK 132

Qy     132 PKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAP 191
           ||||||::|||||||||||||| ||||||||||||||||||||||||||| ||||:||
Db     133 PKNATVMVWIYGGGFQTGTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLAFPGNPDAP 192

Qy     192 GNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQ 251
           |||||||||||||||:|||||||||||:|:|||||||||||||| | |: |||||||:
Db     193 GNMGLFDQQLALQWVQRNIAAFGGNPKSITIFGESAGAASVSLHLLCPQSYPLFTRAILE 252

Qy     252 SGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYG 311
           ||| ||||||    |||||||| ||| ||||:||| |:||||||:||||||| || ||:|
Db     253 SGSSNAPWAVKHPEEARNRTLTLAKFTGCSKENEMEMIKCLRSKDPQEILRNERFVLPSD 312

Qy     312 TPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNS 371
           : ||:|||||||||||||  ||:||: || ||||||||||| ||||||||||||:|
Db     313 SILSINFGPTVDGDFLTDMPHTLLQLGKVKKAQILVGVNKDEGTAFLVYGAPGFSKDNDS 372

Qy     372 IITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPAL 431
           :|||||||||| ::|||||  |||::||:| ||: :| || ||:|| ||:|||| |||||
Db     373 LITRKEFQEGLNMYFPGVSRLGKEAVLFYYVDWLGEQSPEVYRDALDDVIGDYNIICPAL 432

Qy     432 EFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEIL 491
           ||||||:|  ||||||:|||||||||||||||||||||||||||| || |||:||||
Db     433 EFTKKFAELENNAFFYFFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLGRRVNYTRAEEIF 492

Qy     492 SRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWT 551
           ||||:| |||||||:|| || ||| |||| |||||||||||| ::| :|||| ||:||
Db     493 SRSIMKTWANFAKYGHPNGTQGNSTMWPVFTSTEQKYLTLNTEKSKIYSKLRAPQCQFWR 552

Qy     552 SFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           ||||||||||:||| | |||||||||:||||||:|||||||||||||  |
Db     553 LFFPKVLEMTGDIDETEQEWKAGFHRWSNYMMDWQNQFNDYTSKKESCTAL 603
```

RESULT 4
ACRYE

acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric
N;Alternate names: acetylcholinesterase, asymmetric form
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 15-Sep-2000
C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S
Nature 319, 407-409, 1986
A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from :
A;Reference number: A00773; MUID:86118676; PMID:3753747
A;Accession: A00773
A;Molecule type: mRNA
A;Residues: 'NS',11-596 <SCH>
A;Cross-references: GB:X03439; NID:g64389
A;Experimental source: electric organ
A;Note: parts of this sequence, including the amino and carboxyl ends of the mature p
R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.
Fed. Proc. 45, 2976-2981, 1986
A;Title: Primary structure of acetylcholinesterase: implications for regulation and i
A;Reference number: A60820; MUID:87054662; PMID:3536598
A;Accession: A60820
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 22-596 <SC2>
R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.
J. Biol. Chem. 263, 18979-18987, 1988
A;Title: Multiple messenger RNA species give rise to the structural diversity in acet
A;Reference number: A92701; MUID:89066695; PMID:3198606
A;Accession: A31962
A;Molecule type: mRNA
A;Residues: 1-23 <SC3>
A;Cross-references: EMBL:X03439; NID:g64389
A;Experimental source: clones AChE-11 and AChE-18
A;Note: revision to sequence A00773
A;Accession: B31962
A;Molecule type: DNA; mRNA
A;Residues: 499-565 <SC4>
A;Cross-references: GB:X03439; NID:g64389
A;Experimental source: clone AChE-1
R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
J. Biol. Chem. 260, 12185-12189, 1985
A;Title: Primary structures of the catalytic subunits from two molecular forms of ace
A;Reference number: A23902; MUID:86Q08285; PMID:3900071
A;Accession: A23902
A;Molecule type: protein
A;Residues: 22,'B',24-45;214-237 <MAC>
A;Note: active site Ser identification
R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torped
A;Reference number: A41117; MUID:91296772; PMID:2068091
A;Accession: B41117
A;Molecule type: protein
A;Residues: 100-108 <KRE>
A;Note: substrate binding site
R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
Neuron 4, 289-301, 1990
A;Title: Single gene encodes glycophospholipid-anchored and asymmetric acetylcholines
A;Reference number: PS0113; MUID:90166618; PMID:2306366
A;Accession: S15677
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 557-596 <MAU>
A;Cross-references: EMBL:X56516
R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
J. Biol. Chem. 261, 13565-13570, 1986
A;Title: Profile of the disulfide bonds in acetylcholinesterase.
A;Reference number: A43099; MUID:87008586; PMID:3759980
A;Contents: annotation; disulfide bonds
R;Sussman, J.L.; Harel, M.; Silman, I.
submitted to the Brookhaven Protein Data Bank, October 1991
A;Reference number: A50061; PDB:1ACE
A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481,511-555
R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Toker, L.; Silman, I

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Science 253, 872-879, 1991
A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic
A;Reference number: A43098; MUID:91343928; PMID:1678899
A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481,511-555 of
C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a
holinesterase occurs on the outer surfaces of cell membranes, including those of erythro
C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of
C;Function:
A;Description: hydrolyzes acetylcholine to choline and acetate
A;Pathway: neurotransmitter degradation
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane pro
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
F;51-551/Domain: cholinesterase homology <CHE>
F;80,478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;88-115,275-286,423-542/Disulfide bonds: #status experimental
F;105/Binding site: substrate (Trp) #status experimental
F;221/Active site: Ser #status experimental
F;348,461/Active site: Glu, His #status predicted
F;437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;593/Disulfide bonds: interchain #status experimental

  Query Match           55.0%;  Score 1791.5;  DB 1;  Length 596;
  Best Local Similarity  53.2%;  Pred. No. 5.2e-128;
  Matches  314;  Conservative  111;  Mismatches  160;  Indels    5;  Gaps    3;

Qy      13 LFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFK 72
           |   ::||      |:|  ::: ||:||| |  : |    ::||||||:|:||:| :||:
Db      12 LLHLVVLCQ--ADDHSE--LLVNTKSGKVMGTRVPVLSSHISAFLGIPFAEPPVGNMRFR 67

Qy      73 KPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKP 132
           :|:    || :|||: | |:| | :|: |||| |||||||| ::|||||||||:|:|:|:|
Db      68 RPEPKKPWSGVWNASTYPNNCQQYVDEQFPGFSGSEMWNPNREMSEDCLYLNIWVPSPRP 127

Qy     133 KNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPG 192
           |: ||::||||||| :|:|:| ||:||:||  | |::||::||||| ||||| |: ||||
Db     128 KSTTVMVWIYGGGFYSGSSTLDVYNGKYLAYTEEVVLVSLSYRVGAFGFLALHGSQEAPG 187

Qy     193 NMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQS 252
           |:|| ||::||||| ||  |||:||:||:|||||| ||| :|:||||  || ||||||
Db     188 NVGLLDQRMALQWVHDNIQFFGGDPKTVTIFGESAGGASVGMHILSPGSRDLFRRAILQS 247

Qy     253 GSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGT 312
           || | |||  |: | | | : | :   |:  :: |:| ||| | |||::  |  |:|: :
Db     248 GSPNCPWASVSVAEGRRRAVELGRNLNCNLNSDEELIHCLREKKPQELIDVEWNVLPFDS 307

Qy     313 PLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSI 372
           :| | :||:|     : :|  | |||||||:|||||||::||:|||||||||: |
Db     308 IFRFSFVPVIDGEFFPTSLESMLNSGNFKKTQILLGVNKDEGSFFLLYGAPGFSKDSESK 367

Qy     373 ITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALE 432
           |:|::|  |:|:  |  :: | :::   ||||:||      |: | |:|||:| ||| :
Db     368 ISREDFMSGVKLSVPHANDLGLDAVTLQYTDWMDDNNGIKNRDGLDDIVGDHNVICPLMH 427

Qy     433 FTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILS 492
           |  |::::||  : |:| ||:| | |||||||:|||||||||||| :  |||  || ||
Db     428 FVNKYTKFGNGTYLYFFNHRASNLVWPEWMGVIHGYEIEFVFGLPLVKELNYTAEEEALS 487

Qy     493 RSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTS 552
           | |:  || ||| |||||  :  : ||:| : |||:: ||||  ::  :|| | | ||
Db     488 RRIMHYWATFAKTGNPNEPHSQESKWPLFTTKEQKFIDLNTEPMKVHQRLRVQMCVFWNQ 547

Qy     553 FFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           | ||:| |  ||||| :||  ||||::||| |||||: | |: |||  |
Db     548 FLPKLLNATETIDEAERQWKTEFHRWSSYMMHWKNQFDHY-SRHESCAEL 596


RESULT 5
A38868
acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 23-Apr-1993 #sequence_revision 15-Nov-1996 #text_change 11-Jun-1999
C;Accession: A38868; A29682; S15696; A25650
R;Massoulie, J.; Bon, S.
submitted to the EMBL Data Library, June 1992
A;Reference number: A38868
A;Accession: A38868
A;Molecule type: mRNA
A;Residues: 1-599 <MAS>
A;Cross-references: EMBL:X05497; NID:g64414; PIDN:CAA29047.1; PID:g64415
R;Sikorav, J.L.; Krejci, E.; Massoulie, J.
EMBO J. 6, 1865-1873, 1987
A;Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structur
A;Reference number: A29682; MUID:88004392; PMID:2820709
A;Accession: A29682
A;Molecule type: mRNA
A;Residues: 1-40,'G',42-226,'G',228-272,'G',274-284,'E',286-420,'N',422-599 <SIK>
A;Cross-references: EMBL:X05497
R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund
EMBO J. 7, 2983-2993, 1988
A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torped
A;Reference number: S01293; MUID:89030590; PMID:3181125
A;Accession: S15696
A;Molecule type: mRNA
A;Residues: 526-599 <SI2>
A;Cross-references: EMBL:X13172; NID:g64416; PIDN:CAA31570.1; PID:g64417
A;Experimental source: clone pAChE2
R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt
inesterase.
A;Reference number: A91370; MUID:87080761; PMID:3792544
A;Accession: A25650
A;Molecule type: protein
A;Residues: 25-40,'G',42-47 <BON>
C;Genetics:
A;Gene: AChE
C;Function:
A;Description: hydrolyzes acetylcholine to choline and acetate
A;Pathway: neurotransmitter degradation
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotr
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-599/Product: acetylcholinesterase #status predicted <MAT>
F;54-554/Domain: cholinesterase homology <CHE>
F;83,440,481,557/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;91-118,278-289,426-545/Disulfide bonds: #status predicted
F;224,351,464/Active site: Ser, Glu, His #status predicted
F;596/Disulfide bonds: interchain #status predicted

  Query Match           54.9%;  Score 1789.5;  DB 1;  Length 599;
  Best Local Similarity  53.1%;  Pred. No. 7.4e-128;
  Matches  311;  Conservative  116;  Mismatches  158;  Indels    1;  Gaps    1;

Qy      17 LLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQS 76
           ||  ::: ::  : :::: ||:|||    : |    ::||||||:|:||:| :||::|:
Db      15 LLHLVVLCQADDDSELLVNTKSGKVMRTRIPVLSSHISAFLGIPFAEPPVGNMRFRRPEP 74

Qy      77 LTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNAT 136
             || :|||: | |:| | :|: |||| |||||||| ::|||||||||:|:|:|:||:||
Db      75 KKPWSGVWNASTYPNNCQQYVDEQFPGFPGSEMWNPNREMSEDCLYLNIWVPSPRPKSAT 134

Qy     137 VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGL 196
           |::||||||| :|:|:| ||:||:||  | |::||::||||| ||||| |: ||||||||
Db     135 VMLWIYGGGFYSGSSTLDVYNGKYLAYTEEVVLVSLSYRVGAFGFLALHGSQEAPGNMGL 194

Qy     197 FDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFN 256
           ||::||||| ||  |||:||:|||||||||| ||| :|:||||| || |||||:||| |
Db     195 LDQRMALQWVHDNIQFFGGDPKTVTLFGESAGRASVGMHILSPGSRDLFRRAILQSGSPN 254

Qy     257 APWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSV 316
           |||  |: | | | : | :   |:  :: ::|:||| | |||::  |  |:|: :
Db     255 CPWASVSVAEGRRRAVELRRNLNCNLNSDEDLIQCLREKKPQELIDVEWNVLPFDSIFRF 314

Qy     317 NFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRK 376
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          :| | :||:|     : :|  | |||||||:|||||||::||:|||||||||: | |:|:
Db    315 SFVPVIDGEFFPTSLESMLNAGNFKKTQILLGVNKDEGSFFLLYGAPGFSKDSESKISRE 374

Qy    377 EFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKK 436
          :|  |:|:  |  :: | ::   ||||:||      |: | |:|||:| ||| : |  |
Db    375 DFMSGVKLSVPHANDLGLDAVTLQYTDWMDDNNGIKNRDGLDDIVGDHNVICPLMHFVNK 434

Qy    437 FSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIV 496
          ::::||  : |:| ||:| | |||||||:||||||||||||| :  |||  || ||| |:
Db    435 YTKFGNGTYLYFFNHRASNLVWPEWMGVIHGYEIEFVFGLPLVKELNYTAEEEALSRRIM 494

Qy    497 KRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPK 556
            || ||| |||||  :  : ||:| : |||:: |||| ::  :|| | | ||  | ||
Db    495 HYWATFAKTGNPNEPHSQESKWPLFTTKEQKFIDLNTEPIKVHQRLRVQMCVFWNQFLPK 554

Qy    557 VLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
          :|  |  ||||| :||  ||||::||| |||||: | |: |:|  |
Db    555 LLNATETIDEAERQWKTEFHRWSSYMMHWKNQFDQY-SRHENCAEL 599


RESULT 6
A39256
acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1999
C;Accession: A39256; S03959
R;Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw
Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
A;Title: Molecular cloning and construction of the coding region for human acetylcholine
A;Reference number: A39256; MUID:91088577; PMID:2263619
A;Accession: A39256
A;Molecule type: mRNA; DNA
A;Residues: 1-614 <SOR>
A;Cross-references: GB:M55040; NID:g177974; PIDN:AAA68151.1; PID:g177975
A;Note: this sequence represents composite of clones including clone ABGACHE from adult
nce should represent an authentic brain splice form
R;Chhajlani, V.; Derr, D.; Earles, B.; Schmell, E.; August, T.
FEBS Lett. 247, 279-282, 1989
A;Title: Purification and partial amino acid sequence analysis of human erythrocyte acet
A;Reference number: S03959; MUID:89232136; PMID:2714437
A;Accession: S03959
A;Molecule type: protein
A;Residues: 256-266,'Y',268-273;306-308,'X',310-313,'X',315-316,'D',318-323,'D',325-326;
Y',532-551 <CHH>
A;Experimental source: erythrocytes
A;Note: this form was a disulfide-linked homodimer
C;Genetics:
A;Gene: GDB:ACHE; YT
A;Cross-references: GDB:118746; OMIM:100740
A;Map position: 7q22-7q22
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidyl
F;63-569/Domain: cholinesterase homology <CHE>

  Query Match             52.1%;  Score 1698.5;  DB 2;  Length 614;
  Best Local Similarity   52.3%;  Pred. No. 6.3e-121;
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Qy      17 LLLCML---IGKSHTED-DIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFK 72
           ||| :|   :|    || ::::  : |::||: |   || |:||||||:|:||:|  ||
Db      20 LLLWLLGGGVGAEGREDAELLVTVRGGRLRGIRLKTPGGPVSAFLGIPFAEPPMGPRRFL 79

Qy      73 KPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKP 132
           |:    || : :|| : : | | :|  :||| |:|||||| :|||||||||||| | |:|
Db      80 PPEPKQPWSGVVDATTFQSVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRP 139

Qy     133 KNAT-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAP 191
           : | ||:|||||| :| ||| ||||:|| : || ::|||||||| |||||||: |||
Db     140 TSPTPVLVWIYGGGFYSGASSLDVYDGRFLVQAERTVLVSMNYRVGAFGFLALPGSREAP 199

Qy     192 GNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQ 251
           ||:|| ||:|||||||:|:|||||:| |||||||||||||| :||||| |  || ||:||
Db     200 GNVGLLDQRLALQWVQENVAAFGGDPTSVTLFGESAGAASVGMHLLSPPSRGLFHRAVLQ 259

Qy     252 SGSFNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAFV 307
           ||: | |||   | ||| |   || | ||    :  |:||:: ||| :  | :: :|  |
Db     260 SGAPNGPWATVGMGEARRRATQLAHLVGCPPGGTGGNDTELVACLRTRPAQVLVNHEWHV 319

Qy     308 VPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSK 367
           :|  :   :| | |||||||:| |: |:  | |   |:|||| ||||::|||||||||||
Db     320 LPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLVGVVKDEGSYFLVYGAPGFSK 379

Qy     368 DNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFI 427
           || |:|:| ||  |:::  | ||:   |::: |||||:  : |   |||| |||||:| :
Db     380 DNESLISRAEFLAGVRVGVPQVSDLAAEAVVLHYTDWLHPEDPARLREALSDVVGDHNVV 439

Qy     428 CPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKA 487
           ||  :  : :  |   : | ||||:| | || |||| |||||||:||:||:   |||
Db     440 CPVAQLAGRLAAQGARVYAYVFEHRASTLSWPLWMGVPHGYEIEFIFGIPLDPSRNYTAE 499

Qy     488 EEILSRSIVKRWANFAKYGNPNETQN-NSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQ 546
           |:| :: ::: |||||:.|:||| ::  :  || : :  |:|:::|:     :   ||||
Db     500 EKIFAQRLMRYWANFARTGDPNEPRDPKAPQWPPYTAGAQQYVSLDLRPLEVRRGLRAQA 559

Qy     547 CRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           | ||  | ||:|  |  :|||| :||| |||| ::||: |||||: | ||:: |  |
Db     560 CAFWNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQDRCSDL 614


RESULT 7
JH0811
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Jun-1999
C;Accession: JH0811
R;Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.
J. Neurochem. 60, 337-346, 1993
A;Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of
A;Reference number: JH0811; MUID:93107932; PMID:8417155
A;Accession: JH0811
A;Molecule type: mRNA
A;Residues: 1-614 <LEG>
A;Cross-references: GB:S50879; NID:g262092; PIDN:AAB24586.1; PID:g262093
A;Experimental source: striatum
C;Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
F;63-569/Domain: cholinesterase homology <CHE>
F;100-127,288-303,440-560/Disulfide bonds: #status predicted
F;234,365,478/Active site: Ser, Glu, His #status predicted
F;296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             51.9%;  Score 1693.5;  DB 2;  Length 614;
  Best Local Similarity   52.8%;  Pred. No. 1.5e-120;
  Matches  315;  Conservative  103;  Mismatches  168;  Indels   11;  Gaps    5;

Qy      16 FLLLCMLIGKSHTE----DDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRF 71
           |||| :| | :  |      :::  : |::||: |   || |:|||||:|:||:|  ||
Db      19 FLLLSLLGGGARAEGREDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRF 78

Qy      72 KKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPK 131
           |:    || | :|| : | | | :|  :||| |:|||||| :|||||||||| | |:
Db      79 MPPEPKRPWSGILDATTFQNVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPR 138

Qy     132 PKNAT-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEA 190
           | : | |||||||||| :| ||| ||||:|||:|| ::|||||||| ||||||: ||
Db     139 PTSPTPVLIWIYGGGFYSGASSLDVYDGRFLAQVEGTVLVSMNYRVGTFGFLALPGSREA 198

Qy     191 PGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAIL 250
           |||:|| ||:|||||||:|||||||:| |||||||||||||| :|:|| | ||| ||:|
Db     199 PGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSLFHRAVL 258

Qy     251 QSGSFNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAF 306
           |||: | |||  | ||| |   ||:| ||    :  |:||:| ||| :  |::: :|
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Db    259 QSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTELISCLRTRPAQDLVDHEWH 318

Qy    307 VVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFS 366
Db    319 VLPQESIFRFSFVPVVDGDFLSDTPDALINTGDFQDLQVLVGVVKDEGSYFLVYGVPGFS 378

Qy    367 KDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNF 426
Db    379 KDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPAHLRDAMSAVVGDHNV 438

Qy    427 ICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTK 486
Db    439 VCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDPSLNYTV 498

Qy    487 AEEILSRSIVKRWANFAKYGNPNETQNN-STSWPVFKSTEQKYLTLNTESTRIMTKLRAQ 545
Db    499 EERIFAQRLMQYWTNFARTGDPNDPRDSKSPRWPPYTTAAQQYVSLNLKPLEVRRGLRAQ 558

Qy    546 QCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
Db    559 TCAFWNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQERCSDL 614
```

RESULT 8
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999
C;Accession: JH0314
R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
A;Reference number: JH0314; MUID:90380429; PMID:2400605
A;Accession: JH0314
A;Molecule type: mRNA
A;Residues: 1-614 <RAC>
A;Cross-references: EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845
A;Experimental source: brain
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; r
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-614/Product: acetylcholinesterase #status predicted <MAT>
F;63-569/Domain: cholinesterase homology <CHE>
F;100-127,288-303,440-560/Disulfide bonds: #status predicted
F;234/Active site: Ser #status predicted
F;296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

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  Query Match             51.9%;  Score 1692.5;  DB 2;  Length 614;
  Best Local Similarity   52.1%;  Pred. No. 1.8e-120;
  Matches  314;  Conservative  106;  Mismatches  172;  Indels   11;  Gaps    5;

Qy     10 IRFLFWFLLLCMLIGKSHTE----DDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPP 65
Db     13 LAFPLLFLLLSLLGGGARAEGREDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPP 72

Qy     66 LGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNV 125
Db     73 VGSRRFMPPEPKRPWSGVLDATTFQNVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNV 132

Qy    126 WIPAPKPKNAT-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLAL 184
Db    133 WTPYPRPASPTPVLIWIYGGGFYSGAASLDVYDGRFLAQVEGAVLVSMNYRVGTFGFLAL 192

Qy    185 PGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSL 244
Db    193 PGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSL 252

Qy    245 FTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEI 300
Db    253 FHRAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTELIACLRTRPAQDL 312

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360

Db    313 VDHEWHVLPQESIFRFSFVPVVDGDFLSDTPEALINTGDFQDLQVLVGVVKDEGSYFLVY 372

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
Db    373 GVPGFSKDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPTHLRDAMSAV 432

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
Db    433 VGDHNVVCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDP 492

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNN-STSWPVFKSTEQKYLTLNTESTRIM 539
Db    493 SLNYTTEERIFAQRLMKYWTNFARTGDPNDPRDSKSPQWPPYTTAAQQYVSLNLKPLEVR 552

Qy    540 TKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599
Db    553 RGLRAQTCAFWNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQERC 611

Qy    600 VGL 602
Db    612 SDL 614
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RESULT 9
S48724
acetylcholinesterase - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
C;Accession: S48724
R;Jbilo, O.; L'Hermite, Y.; Talesa, V.; Toutant, J.P.; Chatonnet, A.
Eur. J. Biochem. 225, 115-124, 1994
A;Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit
A;Reference number: S48724; MUID:95010096; PMID:7925428
A;Accession: S48724
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-584 <JBI>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: glycoprotein
F;32-539/Domain: cholinesterase homology <CHE>

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  Query Match             50.3%;  Score 1639;  DB 2;  Length 584;
  Best Local Similarity   51.5%;  Pred. No. 1.9e-116;
  Matches  299;  Conservative  106;  Mismatches  168;  Indels    8;  Gaps    5;

Qy     29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
Db      5 DPELLVTVRGGRLRGLRLKAPGGPVSAFLGIPFEEPPVGPRRFLPPEPKRPWAGVLDATA 64

Qy     89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNAT-VLIWIYGGGFQ 147
Db     65 FQSVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPTSPTPVLVWIYGGGFY 124

Qy    148 TGTSSLHVYDGKFLARVERVIVVSM-NYRVGALGFLALPGNPEAPGNMGLFDQQLALQWV 206
Db    125 SGASSLDVYYGRFLVQAEGTVLVAMHNYRVGAFGFTCLPGSREAPGNVGLLDQRLALQWV 184

Qy    207 QKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYE 266
Db    185 QENVAAFGGDPASVTLFGESAGAASVGLHLLSPPSRGLFHRAVLQSGAPNGPWATVGVGE 244

Qy    267 ARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTV 322
Db    245 ARRRATLLARLVVCPPGGAGGNDTELVACLRTRPAQDLVDHEWRVLPQESIFRFSFVPVV 304

Qy    323 DGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGL 382
Db    305 DGDFLSDTPEALINAGDFQGLQVLVGVVKDEGTYFLVYGAPGFSKDNESFISRAQFLAGV 364

Qy    383 KIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGN 442
Db    365 RVGVPQASDLAAEAVVLHYTDWLHPEDPARLRDALSDVVGDHNVVCPVAQLAGRLAAQGA 424
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Qy     443 NAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANF 502
Db     425 RVYAYVFEHRASTLSWPLWMGVPHGYEIEFIFGLPLEPSLNYTEEERIFAQRLMRYWANF 484

Qy     503 AKYGNPNETQN-NSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMT 561
Db     485 ARTGDPNEPRDAKAPQWPPYTAGAQQYVSLNLRPLEVRRGLRAQACAFWNRFLPKLLSAT 544

Qy     562 GNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
Db     545 DTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQDRCSDL 584


RESULT 10
S10712
acetylcholinesterase (EC 3.1.1.7) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 12-May-1995
C;Accession: S10712; A39734; B39734; B25650
R;Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K
FEBS Lett. 266, 123-127, 1990
A;Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its
A;Reference number: S10712; MUID:90306335; PMID:2365060
A;Accession: S10712
A;Molecule type: protein
A;Residues: 1-583 <DOC>
A;Experimental source: fetal serum
R;Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.
J. Biol. Chem. 266, 7481-7487, 1991
A;Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit dis
A;Reference number: A39734; MUID:91210255; PMID:2019579
A;Accession: A39734
A;Molecule type: protein
A;Residues: 1-15,'R',17-38;225-235,'X',237-244;248-264,'X',266-273;365-380;396-404,'X',4
A;Experimental source: brain, erythrocyte
A;Accession: B39734
A;Molecule type: protein
A;Residues: 1-38 <RO2>
A;Experimental source: fetal serum
R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu
inesterase.
A;Reference number: A91370; MUID:87080761; PMID:3792544
A;Accession: B25650
A;Molecule type: protein
A;Residues: 'XS',3-12 <BON>
A;Experimental source: caudate nucleus
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;32-538/Domain: cholinesterase homology <CHE>
F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Active site: Ser #status predicted

  Query Match             50.2%;  Score 1636.5;  DB 2;  Length 583;
  Best Local Similarity   51.7%;  Pred. No. 3e-116;
  Matches  300;  Conservative  103;  Mismatches  170;  Indels    7;  Gaps    4;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
Db       5 DPELLVMVRGGELRGLRLMAPRGPVSAFLGIPFAEPPVGPRRFLPPEPKRPWPGVLNATA 64

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNAT-VLIWIYGGGFQ 147
Db      65 FQSVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPSSPTPVLVWIYGGGFY 124

Qy     148 TGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQ 207
Db     125 SGASSLDVYDGRFLVQAEGTVLVSMNYRVGAFGFLALPGSREAPGNVGLLDQRLALQSVQ 184

Qy     208 KNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEA 267
Db     185 ENVAAFGGDPTSVTLFGESAGAASVGMHLLSPPSRGLFHRAVLQSGAPNGPWATVGVGEA 244

Qy     268 RNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVD 323
Db     245 RRRATLLARLVGCPPGGAGGNDTELVACLRARPAQDLVDHEWRVLPQEHVFRFSFVPVVD 304

Qy     324 GDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLK 383
Db     305 GDFLSDTPEALINAGDFVGLQVLVGVVKDEGSYFLVYGAPGFSKDNESLISRAQFLAGVR 364

Qy     384 IFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNN 443
Db     365 VGVPQASDLAAEAVVLHYTDWLHPEDPARWREALSDVVGDHNVVCPVAQLAGRLAAQGAR 424

Qy     444 AFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFA 503
Db     425 VYAYIFEHRASTLSWPLWMGVPHGYEIEFIFGLPLEPSLNYTIEERTFAQRLMRYWANFA 484

Qy     504 KYGNPNETQ-NNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTG 562
Db     485 RTGDPNDPRAPKAPQWPPYTAGAQQYVSLNLRPLGVPQASRAQACAFWNRFLPKLLNATD 544

Qy     563 NIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
Db     545 TLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQDRCSDL 583


Search completed: January 30, 2003, 11:25:43
Job time : 24 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 30, 2003, 11:24:50 ; Search time 14 Seconds
(without alignments)
1783.482 Million cell updates/sec

Title: US-09-748-739A-2
Perfect score: 3260
Sequence: 1 MDSKVTIICIRFLFWFLLLC.....MDWKNQFNDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	3239	99.4	602	1	CHLE_HUMAN	P06276	homo sapien
2	2855.5	87.6	581	1	CHLE_RABIT	P21927	oryctolagus
3	2774	85.1	574	1	CHLE_HORSE	P81908	equus cabal
4	2593	79.5	603	1	CHLE_MOUSE	Q03311	mus musculu
5	1777	54.5	633	1	ACES_ELEEL	O42275	electrophor
6	1766.5	54.2	634	1	ACES_BRARE	Q9dde3	brachydanio
7	1698.5	52.1	614	1	ACES_HUMAN	P22303	homo sapien
8	1693.5	51.9	614	1	ACES_RAT	P37136	rattus norv
9	1692.5	51.9	614	1	ACES_MOUSE	P21836	mus musculu
10	1683	51.6	611	1	ACES_FELCA	O62763	felis silve
11	1674	51.3	613	1	ACES_BOVIN	P23795	bos taurus
12	1654	50.7	586	1	ACES_TORCA	P04058	torpedo cal
13	1654	50.7	590	1	ACES_TORMA	P07692	torpedo mar
14	1649.5	50.6	584	1	ACES_RABIT	Q29499	oryctolagus
15	1614	49.5	581	1	ACES_BUNFA	Q92035	bungarus fa
16	1466	45.0	767	1	ACES_CHICK	P36196	gallus gall
17	1153	35.4	620	1	ACE1_CAEBR	Q27459	caenorhabdi
18	1142	35.0	620	1	ACE1_CAEEL	P38433	caenorhabdi
19	1140.5	35.0	629	1	ACES_LEPDE	Q27677	leptinotars
20	1059.5	32.5	664	1	ACES_ANOST	P56161	anopheles s
21	1044	32.0	649	1	ACES_DROME	P07140	drosophila
22	1014.5	31.1	338	1	ACES_MYXGL	Q92081	myxine glut
23	901	27.6	337	1	CHL2_BRALA	Q95001	branchiosto
24	896	27.5	357	1	CHL1_BRALA	Q95000	branchiosto
25	754	23.1	532	1	EST2_RABIT	P14943	oryctolagus
26	753	23.1	141	1	CHLE_MACMU	P32751	macaca mula
27	733	22.5	599	1	BAL_MOUSE	Q64285	mus musculu
28	731.5	22.4	561	1	EST1_MESAU	Q64419	mesocricetu
29	729	22.4	612	1	BAL_RAT	P07882	rattus norv
30	728	22.3	597	1	BAL_BOVIN	P30122	bos taurus
31	724.5	22.2	554	1	ESTN_MOUSE	P23953	mus musculu
32	724	22.2	141	1	CHLE_PIG	P32752	sus scrofa
33	721	22.1	141	1	CHLE_BOVIN	P32749	bos taurus
34	721	22.1	141	1	CHLE_SHEEP	P32753	ovis aries
35	717	22.0	565	1	ES10_RAT	P16303	rattus norv
36	713.5	21.9	562	1	ES22_MOUSE	Q64176	mus musculu
37	711	21.8	742	1	BAL_HUMAN	P19835	homo sapien
38	707	21.7	141	1	CHLE_CANFA	P32750	canis famil
39	701.5	21.5	557	1	SASB_ANAPL	Q04791	anas platyr
40	700.5	21.5	567	1	EST1_HUMAN	P23141	homo sapien
41	700	21.5	561	1	EST3_RAT	Q63108	rattus norv
42	699.5	21.5	549	1	EST1_RAT	P10959	rattus norv
43	692	21.2	561	1	EST4_RAT	Q64573	rattus norv
44	690.5	21.2	566	1	EST1_PIG	Q29550	sus scrofa
45	690	21.2	561	1	EST5_RAT	Q63010	rattus norv

ALIGNMENTS

RESULT 1
CHLE_HUMAN
ID CHLE_HUMAN STANDARD; PRT; 602 AA.
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN BCHE OR CHE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90212557; PubMed=2322535;
RA Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.;
RT "Structure of the gene for human butyrylcholinesterase. Evidence for
RT a single copy.";
RL Biochemistry 29:124-131(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal;
RX MEDLINE=87231856; PubMed=3035536;
RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;
RT "Isolation and characterization of full-length cDNA clones coding for
RT cholinesterase from fetal human tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88016155; PubMed=3477799;
RA McTiernan C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;
RT "Brain cDNA clone for human cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.;
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.;

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RT   "Location of disulfide bonds within the sequence of human serum
RT   cholinesterase.";
RL   J. Biol. Chem. 262:12945-12952(1987).
RN   [7]
RP   REVIEW.
RX   MEDLINE=89149758; PubMed=3067729;
RA   Lockridge O.;
RT   "Structure of human serum cholinesterase.";
RL   Bioessays 9:125-128(1988).
RN   [8]
RP   VARIANT ATYPICAL GLY-98.
RX   MEDLINE=89128896; PubMed=2915989;
RA   McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA   van der Spek A.F.L., Lockridge O., la Du B.N.;
RT   "Identification of the structural mutation responsible for the
RT   dibucaine-resistant (atypical) variant form of human serum
RT   cholinesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN   [9]
RP   VARIANT ILE-358.
RX   MEDLINE=96287386; PubMed=8680411;
RA   Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA   Moriwaki K.;
RT   "Mutations of human butyrylcholinesterase gene in a family with
RT   hypocholinesterasemia.";
RL   Hum. Mutat. 6:349-351(1995).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
CC       OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
CC       DISULFIDE BOND.
CC   -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC   -!- DISEASE: MUTANT ALLELES OF CHE1 ARE RESPONSIBLE FOR
CC       HYPOCHOLINESTERASEMIA RESULTING IN SUXAMETHONIUM SENSITIVITY.
CC       HOMOZYGOUS PERSONS SUSTAIN PROLONGED APNEA AFTER ADMINISTRATION
CC       OF THE MUSCLE RELAXANT SUXAMETHONIUM IN CONNECTION WITH SURGICAL
CC       ANESTHESIA.
CC   -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC       ORGANOPHOSPHATE ESTERS.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32391; AAA99296.1; -.
DR   EMBL; M32389; AAA99296.1; JOINED.
DR   EMBL; M32390; AAA99296.1; JOINED.
DR   EMBL; M16541; AAA98113.1; -.
DR   EMBL; M16474; AAA52015.1; -.
DR   EMBL; BC018141; AAH18141.1; -.
DR   PIR; A00772; ACHU.
DR   PIR; A26613; A26613.
DR   PIR; A33769; A33769.
DR   PIR; A33887; A33887.
DR   HSSP; P21836; 1MAA.
DR   Genew; HGNC:983; BCHE.
DR   MIM; 177400; -.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Glycoprotein; Signal; Disease mutation;
KW   Polymorphism.
FT   SIGNAL       1     28
FT   CHAIN       29    602       CHOLINESTERASE.
FT   ACT_SITE    226    226
FT   ACT_SITE    353    353       BY SIMILARITY.
FT   ACT_SITE    466    466       BY SIMILARITY.
FT   DISULFID     93    120
FT   DISULFID    280    291
FT   DISULFID    428    547
FT   DISULFID    599    599       INTERCHAIN.
FT   CARBOHYD     45     45       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    269    269       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    369    369       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    483    483       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    509    509       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    514    514       N-LINKED (GLCNAC. . .).
FT   VARIANT      98     98       D -> G (IN ATYPICAL FORM, DIBUCAINE-
FT                                RESISTANT).
FT                                /FTId=VAR_002360.
FT   VARIANT     271    271       T -> M (IN FLUORIDE-1).
FT                                /FTId=VAR_002361.
FT   VARIANT     358    358       L -> I (IN HYPOCHOLINESTERASEMIA).
FT                                /FTId=VAR_002362.
FT   VARIANT     418    418       G -> V (IN FLUORIDE-2).
FT                                /FTId=VAR_002363.
FT   VARIANT     567    567       A -> T (IN K VARIANT, WITH REDUCED ENZYME
FT                                ACTIVITY).
FT                                /FTId=VAR_002364.
SQ   SEQUENCE   602 AA;  68418 MW;  C9836409D9057F27 CRC64;

  Query Match             99.4%;  Score 3239;  DB 1;  Length 602;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-242;
  Matches  600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MHSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
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Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 2
CHLE_RABIT
ID   CHLE_RABIT     STANDARD;      PRT;   581 AA.
AC   P21927;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
DE   (Pseudocholinesterase).
GN   BCHE.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand;
RX   MEDLINE=90326526; PubMed=2374720;
RA   Jbilo O., Roudani S., Chatonnet A.;
RT   "Complete sequence of rabbit butyrylcholinesterase.";
RL   Nucleic Acids Res. 18:3990-3990(1990).
RN   [2]
RP   SEQUENCE OF 75-215 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91201348; PubMed=2016308;
RA   Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA   Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT   "Use of the polymerase chain reaction for homology probing of
RT   butyrylcholinesterase from several vertebrates.";
RL   J. Biol. Chem. 266:6966-6974(1991).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC       TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC   -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC   -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC       ORGANOPHOSPHATE ESTERS.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X52090; CAA36308.1; -.
DR   EMBL; X52091; CAA36308.1; JOINED.
DR   EMBL; X52092; CAA36308.1; JOINED.
DR   EMBL; M62779; AAA31169.1; -.
DR   PIR; S10255; S10255.
DR   PIR; C39768; C39768.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Glycoprotein; Signal.
FT   SIGNAL        1      8       POTENTIAL.
FT   CHAIN         9    581       CHOLINESTERASE.
FT   ACT_SITE    205    205
FT   ACT_SITE    332    332       BY SIMILARITY.
FT   ACT_SITE    445    445       BY SIMILARITY.
FT   DISULFID     72     99       BY SIMILARITY.
FT   DISULFID    259    270       BY SIMILARITY.
FT   DISULFID    407    526       BY SIMILARITY.
FT   DISULFID    578    578       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     64     64       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    263    263       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    462    462       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    488    488       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    492    492       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    493    493       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   581 AA;  66156 MW;  FE8B199E7B32EB0A CRC64;

  Query Match             87.6%;  Score 2855.5;  DB 1;  Length 581;
  Best Local Similarity   91.4%;  Pred. No. 5.6e-213;
  Matches  531;  Conservative   12;  Mismatches   37;  Indels    1;  Gaps    1;

Qy      21 MLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKW 80
           |:   |||| |:|| |||||::||:|| |||||||||||||||||||||||||||||||||
Db       1 MVTRSSHTE-DVIITTKNGRIRGINLPVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKW 59

Qy      81 SDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIW 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||:||
Db      60 SDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPTPKPKNATVMIW 119

Qy     141 IYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQ 200
           |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||||
Db     120 IYGGGFQTGTSSLQVYDGKFLTRVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQ 179

Qy     201 LALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWA 260
           |||||||||||||||||||||||||||||||||||| || |||||||||| ||||
Db     180 LALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPRSHPLFTRAILQSGSSNAPWE 239

Qy     261 VTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGP 320
           | ||:||||||| |||  ||| |||||||||||||| ||||||| |||| : ||||||||
Db     240 VMSLHEARNRTLTLAKFVGCSTENETEIIKCLRNKDAQEILLNEVFVVPFDSLLSVNFGP 299

Qy     321 TVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQE 380
           |||||||||||| ||:||| |||||||||||||||| |||||||||||| ||||||||||
Db     300 TVDGDFLTDMPDTLLQLGQLKKTQILVGVNKDEGTAFLVYGAPGFSKDNTSIITRKEFQE 359

Qy     381 GLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEW 440
           |||||||||||||||||||||||:|||||||| ||||||||||||||||||||||||||||
Db     360 GLKIFFPGVSEFGKESILFHYTDWVDEQRPENYREALDDVVGDYNFICPALEFTKKFSEW 419

Qy     441 GNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWA 500
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||:||||
Db     420 GNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRVNYTKAEEILSRSIMKRWA 479

Qy     501 NFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEM 560
           |||||||| |||||| |||||||||||||||||| || |||||||||||| ||||||||
Db     480 NFAKYGNPNGTQNNSTRWPVFKSTEQKYLTLNTESPRIYTKLRAQQCRFWTLFFPKVLEM 539

Qy     561 TGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVG 601
           |||||||| |||||||||||||| ||| ||||||||| | |
Db     540 TGNIDEAEQEWKAGFHRWNNYMMAWKNHFNDYTSKKERCAG 580


RESULT 3
CHLE_HORSE
ID   CHLE_HORSE     STANDARD;      PRT;   574 AA.
AC   P81908;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE   esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EQ-
DE   BCHE).
GN   BCHE.
OS   Equus caballus (Horse).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RA   Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;
RT   "Amino acid sequence of horse serum butyrycholinesterase.";
RL   (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.
RL   (eds.);
RL   Structure and function of cholinesterases and related proteins,
RL   pp.145-146, Plenum Press, New York and London (1998).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC       TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC   -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC   -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC       ORGANOPHOSPHATE ESTERS.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Glycoprotein.
FT   ACT_SITE    198    198       BY SIMILARITY.
FT   ACT_SITE    325    325       BY SIMILARITY.
FT   ACT_SITE    438    438       BY SIMILARITY.
FT   DISULFID     65     92       BY SIMILARITY.
FT   DISULFID    252    263       BY SIMILARITY.
FT   DISULFID    400    519       BY SIMILARITY.
FT   DISULFID    571    571       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    256    256       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    455    455       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    481    481       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    486    486       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   574 AA;  65641 MW;  07755EE9FB9CB33E CRC64;

  Query Match           85.1%;  Score 2774;  DB 1;  Length 574;
  Best Local Similarity  90.5%;  Pred. No. 1.1e-206;
  Matches  517;  Conservative   20;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      29 EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 88
           |:|||| |||||||||| | ||||||||||||||||||||||||||||||||:||||||
Db       1 EEDIIITTKNGKVRGMNLPVLGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSNIWNATK 60

Qy      89 YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVLIWIYGGGFQT 148
           ||||| || ||||||| |||||||||:||||||||||||||||||||:||||||||||
Db      61 YANSCYQNTDQSFPGFLGSEMWNPNTELSEDCLYLNVWIPAPKPKNATVMIWIYGGGFQT 120

Qy     149 GTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVQK 208
           ||||| |||||||||||||||||||||||||  ||||||||||||||||||||
Db     121 GTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLALSENPEAPGNMGLFDQQLALQWVQK 180

Qy     209 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
           |||||||||:||||||||||||||||||| |  |||||||||| ||||||||||||||
Db     181 NIAAFGGNPRSVTLFGESAGAASVSLHLLSPRSQPLFTRAILQSGSSNAPWAVTSLYEAR 240

Qy     269 NRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
           |||| |||  |||||||||||||||||||||||| ||||| | ||||||||||||||||
Db     241 NRTLTLAKRMGCSRDNETEMIKCLRDKDPQEILLNEVFVVPYDTLLSVNFGPTVDGDFLT 300

Qy     329 DMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPG 388
           |||| ||:|||||:|||||||||||||| |||||||||||||||||||||||||||||||
Db     301 DMPDTLLQLGQFKRTQILVGVNKDEGTAFLVYGAPGFSKDNNSIITRKEFQEGLKIFFPR 360

Qy     389 VSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEWGNNAFFYY 448
           |||||:||||||| ||:|||| ||||||| ||||||| ||||||||:|||| ||:|||||
Db     361 VSEFGRESILFHYMDWLDDQRAENYREALDDVVGDYNIICPALEFTRKFSELGNDAFFYY 420

Qy     449 FEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP 508
           |||||:|||||||||||||||||||||||||| |||:|||||||||:||||||||||||
Db     421 FEHRSTKLPWPEWMGVMHGYEIEFVFGLPLERRVNYTRAEEILSRSIMKRWANFAKYGNP 480

Qy     509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAE 568
           | |||||| |||||||||||||||||| :: |||||||||||| |||||||:||||||||
Db     481 NGTQNNSTRWPVFKSTEQKYLTLNTESPKVYTKLRAQQCRFWTLFFPKVLELTGNIDEAE 540

Qy     569 WEWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599
           ||||||||||||||||||||||||||||||
Db     541 REWKAGFHRWNNYMMDWKNQFNDYTSKKESC 571


RESULT 4
CHLE_MOUSE
ID   CHLE_MOUSE     STANDARD;      PRT;   603 AA.
AC   Q03311;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
DE   (Pseudocholinesterase).
GN   BCHE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90380429; PubMed=2400605;
RA   Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT   "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT   of alternatively spliced mRNA species.";
RL   Neuron 5:317-327(1990).
RN   [2]
RP   SEQUENCE OF 97-237 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91201348; PubMed=2016308;
RA   Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA   Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT   "Use of the polymerase chain reaction for homology probing of
RT   butyrylcholinesterase from several vertebrates.";
RL   J. Biol. Chem. 266:6966-6974(1991).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC       TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC   -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS (EXCEPT ERYTHROCYTES).
CC   -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC       ORGANOPHOSPHATE ESTERS.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M99492; AAA37328.1; -.
DR   PIR; A39768; A39768.
DR   HSSP; P21836; 1MAH.
DR   MGD; MGI:894278; Bche.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
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DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Glycoprotein; Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    603       CHOLINESTERASE.
FT   ACT_SITE    227    227       BY SIMILARITY.
FT   ACT_SITE    354    354       BY SIMILARITY.
FT   ACT_SITE    467    467       BY SIMILARITY.
FT   DISULFID     94    121       BY SIMILARITY.
FT   DISULFID    281    292       BY SIMILARITY.
FT   DISULFID    429    548       BY SIMILARITY.
FT   DISULFID    600    600       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    270    270       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    370    370       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    484    484       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    510    510       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    515    515       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    129    129       R -> P (IN REF. 2).
SQ   SEQUENCE   603 AA;  68521 MW;  719B1B220D1E5367 CRC64;

  Query Match           79.5%;  Score 2593;  DB 1;  Length 603;
  Best Local Similarity  80.4%;  Pred. No. 1.1e-192;
  Matches  475;  Conservative   47;  Mismatches   69;  Indels    0;  Gaps    0;

Qy      12 FLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRF 71
           ||.| |||||  ||||||:| || || |:|||::: | |||||||||||||||||| |||
Db      13 FLLWILLLCMPFGKSHTEEDFIITTKTGRVRGLSMPVLGGTVTAFLGIPYAQPPLGSLRF 72

Qy      72 KKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPK 131
           |||| | || || |||:|||| |||||:|||| |||||||||:|||||||||||  ||
Db      73 KKPQPLNKWPDIHNATQYANSCYQNIDQAFPGFQGSEMWNPNTNLSEDCLYLNVWIRVPK 132

Qy     132 PKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAP 191
           ||||||::|||||||||||||| ||||||||||||||||||||||||||||||| ||||:||
Db     133 PKNATVMVWIYGGGFQTGTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLAFPGNPDAP 192

Qy     192 GNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQ 251
           |||||||||||||||:|||||||||||:|:|||||||||||||| | |: |||||||:
Db     193 GNMGLFDQQLALQWVQRNIAAFGGNPKSITIFGESAGAASVSLHLLCPQSYPLFTRAILE 252

Qy     252 SGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYG 311
           ||| ||||||    ||||||| ||| ||||:||| |:|||||:||||||| || ||:|
Db     253 SGSSNAPWAVKHPEEARNRTLTLAKFTGCSKENEMEMIKCLRSKDPQEILRNERFVLPSD 312

Qy     312 TPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNS 371
           : ||:|||||||||||||  ||:||: || |||||||||||| ||||||||||||:|
Db     313 SILSINFGPTVDGDFLTDMPHTLLQLGKVKKAQILVGVNKDEGTAFLVYGAPGFSKDNDS 372

Qy     372 IITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPAL 431
           :|||||||||| ::|||||  |||:::||:| ||: :| || ||:|| ||:|||| |||||
Db     373 LITRKEFQEGLNMYFPGVSRLGKEAVLFYYVDWLGEQSPEVYRDALDDVIGDYNIICPAL 432

Qy     432 EFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEIL 491
           |||||:| ||||||:|||||||||||||||||||||||||||| || |||:|||| 
Db     433 EFTKKFAELENNAFFYFFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLGRRVNYTRAEEIF 492

Qy     492 SRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWT 551
           ||||:| |||||||:|| || ||| |||| |||||||||| ::| :|||| ||:||
Db     493 SRSIMKTWANFAKYGHPNGTQGNSTMWPVFTSTEQKYLTLNTEKSKIYSKLRAPQCQFWR 552

Qy     552 SFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
            |||||||||:||| | |||||||||:||||||:|||||||||||  |
Db     553 LFFPKVLEMTGDIDETEQEWKAGFHRWSNYMMDWQNQFNDYTSKKESCTAL 603


RESULT 5
ACES_ELEEL
ID   ACES_ELEEL     STANDARD;      PRT;   633 AA.
AC   O42275;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
OS   Electrophorus electricus (Electric eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Electrophoridae; Electrophorus.
OX   NCBI_TaxID=8005;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98070504; PubMed=9407087;
RA   Simon S., Massoulie J.;
RT   "Cloning and expression of acetylcholinesterase from Electrophorus.
RT   Splicing pattern of the 3' exons in vivo and in transfected mammalian
RT   cells.";
RL   J. Biol. Chem. 272:33045-33055(1997).
CC   -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: DIMERS AND COLLAGEN-TAILED FORMS, IN WHICH CATALYTIC
CC       TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM
CC       TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED
CC       FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLQ,
CC       WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS FROM DIMERS.
CC   -!- MISCELLANEOUS: NO OTHER ISOFORMS EXIST. THIS PROTEIN CORRESPONDS
CC       TO THE T ISOFORM IN OTHER SPECIES.
CC   -!- SIMILARITY: BELONGS TO THE CARBOXYLESTERASE TYPE-B FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF030422; AAB86606.1; -.
DR   HSSP; P04058; 1SOM.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW   Neurotransmitter degradation; Glycoprotein.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    633       ACETYLCHOLINESTERASE.
FT   ACT_SITE    225    225       BY SIMILARITY.
FT   ACT_SITE    352    352       BY SIMILARITY.
FT   ACT_SITE    494    494       BY SIMILARITY.
FT   DISULFID     91    118       BY SIMILARITY.
FT   DISULFID    279    290       BY SIMILARITY.
FT   DISULFID    427    579       BY SIMILARITY.
FT   DISULFID    630    630       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    368    368       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    511    511       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    591    591       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   633 AA;  71814 MW;  FC92FE7E4ADB84C3 CRC64;

  Query Match           54.5%;  Score 1777;  DB 1;  Length 633;
  Best Local Similarity  52.4%;  Pred. No. 1.4e-129;
  Matches  328;  Conservative  108;  Mismatches  150;  Indels   40;  Gaps    7;

Qy      12 FLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGT-VTAFLGIPYAQPPLGRLR 70
           |: :|: | :    : |: :: | |: |:|:|  | | ` : | ||||||:|:||||::|
Db      13 FIMFFIHLSI----AQTDPELTIMTRLGQVQGTRLPVPDRSHVIAFLGIPFAEPPLGKMR 68

Qy      71 FKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPA- 129
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Db      69 FKPPEPKKPWNDVFDARDYPSACYQYVDTSYPGFSGTEMWNPNRMMSEDCLYLNVWVPAT 128

Qy     130 PKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPE 189

Db     129 PRPHNLTVMVWIYGGGFYSGSSSLDVYDGRYLAHSEKVVVVSMNYRVSAFGFLALNGSAE 188

Qy     190 APGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAI 249

Db     189 APGNVGLLDQRLALQWVQDNIHFFGGNPKQVTIFGESAGAASVGMHLLSPDSRPKFTRAI 248

Qy     250 LQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVP 309

Db     249 LQSGVPNGPWRTVSFDEARRRAIKLGRLVGCPDGNDTDLIDCLRSKQPQDLIDQEWLVLP 308

Qy     310 YGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDN 369

Db     309 FSGLFRFSFVPVIDGVVFPDTPEAMLNSGNFKDTQILLGVNQNEGSYFLIYGAPGFSKDN 368

Qy     370 NSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICP 429

Db     369 ESLITREDFLQGVKMSVPHANEIGLEAVILQYTDWMDEDNPIKNREAMDDIVGDHNVVCP 428

Qy     430 ALEFTKKFSE----------------WGN------------NAFFYYFEHRSSKLPWPE 460

Db     429 LQHFAKMYAQYSILQGQTGTASQGNLGWGNSGSASNSGNSQVSVYLYMFDHRASNLVWPE 488

Qy     461 WMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTS--- 517

Db     489 WMGVIHGYEIEFVFGLPLEKRLNYTLEEEKLSRRMMKYWANFARTGNPNINVDGSIDSRR 548

Qy     518 -WPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFH 576

Db     549 RWPVFTSTEQKHVGLNTDSLKVHKGLKSQFCALWNRFLPRLLNVTENIDDAERQWKAEFH 608

Qy     577 RWNNYMMDWKNQFNDYTSKKESCVGL 602

Db     609 RWSSYMMHWKNQFDHY-SKQERCTNL 633
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RESULT 6
ACES_BRARE
ID   ACES_BRARE     STANDARD;      PRT;   634 AA.
AC   Q9DDE3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   ACHE.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20576389; PubMed=11016933;
RA   Bertrand C., Chatonnet A., Takke C., Yan Y., Postlethwait J.,
RA   Toutant J.-P., Cousin X.;
RT   "Zebrafish acetylcholinesterase is encoded by a single gene localized
RT   on linkage group 7. gene structure and polymorphism; molecular forms
RT   and expression pattern during development.";
RL   J. Biol. Chem. 276:464-474(2001).
CC   -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: DIMERS AND COLLAGEN-TAILED FORMS, IN WHICH CATALYTIC
CC       TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM
CC       TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED
CC       FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLQ,
CC       WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS FROM DIMERS.
CC   -!- MISCELLANEOUS: NO OTHER ISOFORMS EXIST. THIS PROTEIN CORRESPONDS
CC       TO THE T ISOFORM IN OTHER SPECIES.
CC   -!- SIMILARITY: BELONGS TO THE CARBOXYLESTERASE TYPE-B FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251640; CAC19790.1; -.
DR   HSSP; P04058; 1SOM.
DR   ZFIN; ZDB-GENE-010906-1; ache.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW   Neurotransmitter degradation; Glycoprotein.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    634       ACETYLCHOLINESTERASE.
FT   ACT_SITE    225    225       BY SIMILARITY.
FT   ACT_SITE    352    352       BY SIMILARITY.
FT   ACT_SITE    495    495       BY SIMILARITY.
FT   DISULFID     91    118       BY SIMILARITY.
FT   DISULFID    279    290       BY SIMILARITY.
FT   DISULFID    427    580       BY SIMILARITY.
FT   DISULFID    631    631       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    368    368       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    512    512       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    592    592       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   634 AA;  71998 MW;  47F348EA8A7C1E52 CRC64;
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Query Match 54.2%; Score 1766.5; DB 1; Length 634;
Best Local Similarity 52.7%; Pred. No. 9.2e-129;
Matches 323; Conservative 107; Mismatches 146; Indels 37; Gaps 6;

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Qy      26 SHTEDDIIIATKNGKVRGMNLTVFGGT-VTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIW 84

Db      23 AQAEPDLVVATRLGRVQGTRLPVPDRSHVIAFLGIPYAEPPIGKRRFKRAEPKKPWNNVF 82

Qy      85 NATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWI-PAPKPKNATVLIWIYG 143

Db      83 EAKEFSNACYQFVDTSYPGFPGIEMWNPNRVMSEDCLYLNVWVPPTPRPQNLTVMVWIYG 142

Qy     144 GGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQLAL 203

Db     143 GGFYSGSSSLDVYDGRYLAYTEKVVVVSMNYRVGAFGFLALNGSSDAPGNVGLYDQRLAL 202

Qy     204 QWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTS 263

Db     203 QWVQENIHFFGGNPKQVTIFGESAGAASVGMHVLSPDSRPLFTRAILQSGVPNTPWATVT 262

Qy     264 LYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVD 323

Db     263 FDEARRRTTKLGKLVGCTWGNDTELIDCLRNKHPQELIDQEWQVLPWSSLFRFSFVPVVD 322

Qy     324 GDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQEGLK 383

Db     323 GVFFPDTPDAMISSGNFKYTQILLGVNQDEGSYFLLYGAPGFSKDNESLISREDFLESVK 382

Qy     384 IFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSE---- 439

Db     383 MGVPHANDIGLEAVILQYTDWMDENNGQKNRDAMDDIVGDQNVICPLQHFAKSYAQYAAL 442

Qy     440 ------------WGNN------------AFFYYFEHRSSKLPWPEWMGVMHGYEIEFV 473

Db     443 HAQSSAAAPGTLGWGNSGPTGYNSGNSHGAVYLYLFDHRASNLAWPEWMGVIHGYEIEFV 502
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Qy     474 FGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNPN----ETQNNSTSWPVFKSTEQKYL 529
           ||||||:| |||  || ||| |:: |||||: ||||     | ::   || | : |||:: 
Db     503 FGLPLEKRLNYTAEEEKLSRRIMRYWANFARTGNPNVNTDGTMDSRRRWPQFSANEQKHV 562

Qy     530 TLNTESTRIMTKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQF 589
           ||||  ::   || | |  |  | |::| :| |||: | :|| ||||::||| ||:|| 
Db     563 GLNTEPMKVHKGLRTQFCALWNRFLPRLLNITDNIDDVERQWKVEFHRWSSYMMHWKSQF 622

Qy     590 NDYTSKKESCVGL 602
           : | ||:| |  | 
Db     623 DHY-SKQERCTDL 634


RESULT 7
ACES_HUMAN
ID   ACES_HUMAN     STANDARD;      PRT;   614 AA.
AC   P22303; Q9BXP7; Q16169;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   ACHE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088577; PubMed=2263619;
RA   Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnatt A., Neville L.,
RA   Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA   Zakut H.;
RT   "Molecular cloning and construction of the coding region for human
RT   acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN   [2]
RP   SEQUENCE OF 521-614 FROM N.A.
RX   MEDLINE=21138439; PubMed=11239002;
RA   Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA   Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA   Miller W., Koop B.F.;
RT   "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT   chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL   Nucleic Acids Res. 29:1352-1365(2001).
RN   [3]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=94131004; PubMed=8299725;
RA   Karpel R., Ben Aziz-Aloya R., Sternfeld M., Ehrlich G., Ginzberg D.,
RA   Tarroni P., Clementi F., Zakut H., Soreq H.;
RT   "Expression of three alternative acetylcholinesterase messenger RNAs
RT   in human tumor cell lines of different tissue origins.";
RL   Exp. Cell Res. 210:268-277(1994).
RN   [4]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Erythrocyte;
RX   MEDLINE=89232136; PubMed=2714437;
RA   Chhajlani V., Derr D., Earles B., Schmell E., August T.;
RT   "Purification and partial amino acid sequence analysis of human
RT   erythrocyte acetylcholinesterase.";
RL   FEBS Lett. 247:279-282(1989).
RN   [5]
RP   3D-STRUCTURE MODELING OF 35-574.
RX   MEDLINE=98304745; PubMed=9640563;
RA   Felder C.E., Botti S.A., Lifson S., Silman I., Sussman J.L.;
RT   "External and internal electrostatic potentials of cholinesterase
RT   models.";
RL   J. Mol. Graph. Model. 15:318-327(1997).
RN   [6]
RP   MUTAGENESIS OF CYS-611.
RX   MEDLINE=92084699; PubMed=1748670;
RA   Velan B., Grosfeld H., Kronman C., Leitner M., Gozes Y., Lazar A.,
RA   Flashner Y., Marcus D., Cohen S., Shafferman A.;
RT   "The effect of elimination of intersubunit disulfide bonds on the
RT   activity, assembly, and secretion of recombinant human
RT   acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT   mutant.";
RL   J. Biol. Chem. 266:23977-23984(1991).
RN   [7]
RP   MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX   MEDLINE=92388112; PubMed=1517212;
RA   Shafferman A., Kronman C., Flashner Y., Leitner M., Grosfeld H.,
RA   Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT   "Mutagenesis of human acetylcholinesterase. Identification of
RT   residues involved in catalytic activity and in polypeptide folding.";
RL   J. Biol. Chem. 267:17640-17648(1992).
RN   [8]
RP   VARIANT BLOOD GROUP YT(B).
RX   MEDLINE=93256075; PubMed=8488842;
RA   Bartels C.F., Zelinski T., Lockridge O.;
RT   "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
RT   accounts for YT blood group polymorphism.";
RL   Am. J. Hum. Genet. 52:928-936(1993).
CC   -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- POLYMORPHISM: ACHE IS RESPONSIBLE FOR THE YT BLOOD GROUP SYSTEM.
CC       THE MOLECULAR BASIS OF THE YT(A)=YT1/YT(B)=YT2 BLOOD GROUP
CC       ANTIGENS IS A SINGLE VARIATION IN POSITION 353; HIS-353
CC       CORRESPONDS TO YT(A) AND THE RARE VARIANT WITH ASN-353 TO YT(B).
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55040; AAA68151.1; -.
DR   EMBL; AF312032; AAK21003.1; -.
DR   EMBL; S71129; AAC60618.1; -.
DR   PIR; S03959; S03959.
DR   PIR; A39256; A39256.
DR   PDB; 2CLJ; 04-MAR-98.
DR   SWISS-2DPAGE; P22303; HUMAN.
DR   Genew; HGNC:108; ACHE.
DR   MIM; 100740; -.
DR   MIM; 112100; -.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW   Neurotransmitter degradation; Glycoprotein; Polymorphism;
KW   Blood group antigen; Alternative splicing; 3D-structure.
FT   SIGNAL       1     31       POTENTIAL.
FT   CHAIN       32    614       ACETYLCHOLINESTERASE.
FT   ACT_SITE    234    234
FT   ACT_SITE    365    365
FT   ACT_SITE    478    478
FT   DISULFID    100    127
FT   DISULFID    288    303
FT   DISULFID    440    560
FT   DISULFID    611    611       INTERCHAIN.
FT   CARBOHYD    296    296       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    381    381       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    495    495       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    575    614       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQDRCSDL
FT                                -> GMQGPAGSAGRRGVGARQCNPSLLPLASEAPSTCPGFT
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FT                                   HGEAAPRPGLPLPLLLLHQLLLLFLSHLRRL (IN
FT                                   ISOFORM 2).
FT   VARIANT      333    333         V -> E (IN DBSNP:8286).
FT                                   /FTId=VAR_011934.
FT   VARIANT      353    353         H -> N (IN YT(B) ANTIGEN).
FT                                   /FTId=VAR_002359.
FT   MUTAGEN      234    234         S->A: LOSS OF ACTIVITY.
FT   MUTAGEN      365    365         E->A: LOSS OF ACTIVITY.
FT   MUTAGEN      478    478         H->A: LOSS OF ACTIVITY.
FT   MUTAGEN      206    206         D->N: MISFOLDING, ABSENCE OF SECRETION.
FT   MUTAGEN      435    435         D->N: MISFOLDING, ABSENCE OF SECRETION.
FT   MUTAGEN      611    611         C->A: IMPAIRMENT OF INTERCHAIN DISULFIDE
FT                                   BRIDGE FORMATION.
SQ   SEQUENCE   614 AA;  67796 MW;  B9AA84C77831C302 CRC64;

 Query Match           52.1%;  Score 1698.5;  DB 1;  Length 614;
 Best Local Similarity 52.3%;  Pred. No. 1.6e-123;
 Matches  312;  Conservative  106;  Mismatches  167;  Indels   11;  Gaps    6;

Qy      17 LLLCML---IGKSHTED-DIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFK 72
           ||| :|   :|    || :::: : |::||: |   || |:|||||:|:||:| ||
Db      20 LLLWLLGGGVGAEGREDAELLVTVRGGRLRGIRLKTPGGPVSAFLGIPFAEPPMGPRRFL 79

Qy      73 KPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKP 132
           |:    || : :|| : : | | :|  :||| |:|||||| :|||||||||||| | |:|
Db      80 PPEPKQPWSGVVDATTFQSVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRP 139

Qy     133 KNAT-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAP 191
           : | ||:||||||| :| ||| ||||:|| : || ::|||||||| ||:|||||: |||
Db     140 TSPTPVLVWIYGGGFYSGASSLDVYDGRFLVQAERTVLVSMNYRVGAFGFLALPGSREAP 199

Qy     192 GNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQ 251
           ||:|| ||:|||||||:|:|||||:| |||||||||||||| :|||| |  || ||:||
Db     200 GNVGLLDQRLALQWVQENVAAFGGDPTSVTLFGESAGAASVGMHLLSPPSRGLFHRAVLQ 259

Qy     252 SGSFNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAFV 307
           ||: | |||   : ||| |   || | ||    :  |:||:: ||| :  | :: :|  |
Db     260 SGAPNGPWATVGMGEARRRATQLAHLVGCPPGGTGGNDTELVACLRTRPAQVLVNHEWHV 319

Qy     308 VPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSK 367
           :|  :    :| | ||||||:| |: |:  | |   |:|||| ||||::||||||||||
Db     320 LPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLVGVVKDEGSYFLVYGAPGFSK 379

Qy     368 DNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFI 427
           || |:|:| ||  |::: | ||:   |::: |||||:  : |   |||| |||||:| :
Db     380 DNESLISRAEFLAGVRVGVPQVSDLAAEAVVLHYTDWLHPEDPARLREALSDVVGDHNVV 439

Qy     428 CPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKA 487
           ||  :   : :  |   : | ||||:| | || |||| |||||||:||:||:   |||
Db     440 CPVAQLAGRLAAQGARVYAYVFEHRASTLSWPLWMGVPHGYEIEFIFGIPLDPSRNYTAE 499

Qy     488 EEILSRSIVKRWANFAKYGNPNETQN-NSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQ 546
           |:| :: ::: |||||: |:||| ::  :  || : :  |:|::|:     :   ||||
Db     500 EKIFAQRLMRYWANFARTGDPNEPRDPKAPQWPPYTAGAQQYVSLDLRPLEVRRGLRAQA 559

Qy     547 CRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           | ||  | ||:|  |  :|||| :||| ||||::||: |||||: | ||:: |  |
Db     560 CAFWNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQDRCSDL 614


RESULT 8
ACES_RAT
ID   ACES_RAT       STANDARD;      PRT;   614 AA.
AC   P37136;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   ACHE.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM T).
RX   MEDLINE=93107932; PubMed=8417155;
RA   Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;
RT   "Cloning and expression of a rat acetylcholinesterase subunit:
RT   generation of multiple molecular forms and complementarity with a
RT   Torpedo collagenic subunit.";
RL   J. Neurochem. 60:337-346(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX   MEDLINE=93114454; PubMed=8417973;
RA   Legay C., Bon S., Massoulie J.;
RT   "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT   acetylcholinesterase.";
RL   FEBS Lett. 315:163-166(1993).
CC   -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC       CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-
CC       TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES
CC       OF KNOWN ACHE FORMS.
CC   -!- ALTERNATIVE PRODUCTS: 3 isoforms; T (shown here), H and R; are
CC       produced by alternative splicing. It is not known whether isoform
CC       R is functional.
CC   -!- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND
CC       MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT
CC       LIVER.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S50879; AAB24586.1; -.
DR   EMBL; X70140; CAA49717.1; -.
DR   EMBL; X70141; CAA49718.1; -.
DR   PIR; JH0811; JH0811.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW   Neurotransmitter degradation; Glycoprotein; Alternative splicing.
FT   SIGNAL        1     31       POTENTIAL.
FT   CHAIN        32    614       ACETYLCHOLINESTERASE.
FT   ACT_SITE     234    234       BY SIMILARITY.
FT   ACT_SITE     365    365       BY SIMILARITY.
FT   ACT_SITE     478    478       BY SIMILARITY.
FT   DISULFID     100    127       BY SIMILARITY.
FT   DISULFID     288    303       BY SIMILARITY.
FT   DISULFID     440    560       BY SIMILARITY.
FT   DISULFID     611    611       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     296    296       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     381    381       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     495    495       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     575    614       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQERCSDL
FT                                 -> ATEVPCTCPSPAHGEAAPRPGPALSLSLLFFLFLLHSG
FT                                 LRWL (IN ISOFORM H).
FT   VARSPLIC     575    614       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQERCSDL
FT                                 -> GRRGVGKQGMHKAARVGRTGERKGGKHRM (IN
FT                                 ISOFORM R).
SQ   SEQUENCE   614 AA;  68196 MW;  2EDAE7D46282E7C0 CRC64;

 Query Match           51.9%;  Score 1693.5;  DB 1;  Length 614;
 Best Local Similarity 52.8%;  Pred. No. 3.9e-123;
```

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  Matches  315;  Conservative  103;  Mismatches  168;  Indels   11;  Gaps    5;

Qy      16 FLLLCMLIGKSHTE----DDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRF 71
           |||| :| | :  |       :::  : |::||: |   || |:||||||:|:||:|  ||
Db      19 FLLLSLLGGGARAEGREDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRF 78

Qy      72 KKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPK 131
             |:    || | :|| : | | | :|  :||| |:|||||| :|||||||||| | |:
Db      79 MPPEPKRPWSGILDATTFQNVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPR 138

Qy     132 PKNAT-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEA 190
           | : | |||||||||| :| ||| ||||:|||:||  ::|||||||  |||||||: ||
Db     139 PTSPTPVLIWIYGGGFYSGASSLDVYDGRFLAQVEGTVLVSMNYRVGTFGFLALPGSREA 198

Qy     191 PGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAIL 250
           |||:|| ||:|||||||:|||||||:| |||||||||||||| :|:||  | ||| ||:|
Db     199 PGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSLFHRAVL 258

Qy     251 QSGSFNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAF 306
           |||: | |||  |  ||| |   ||:| ||    :  |:|||:| ||| :  |::: :|
Db     259 QSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTELISCLRTRPAQDLVDHEWH 318

Qy     307 VVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFS 366
           |:|  :    :| | ||||||:| || |:  | |:  |:|||| ||||::|||| ||||
Db     319 VLPQESIFRFSFVPVVDGDFLSDTPDALINTGDFQDLQVLVGVVKDEGSYFLVYGVPGFS 378

Qy     367 KDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNF 426
           ||| |:|:| :| ·|::|  |  |:   |::: |||||:  : | : |:|:  ||||:|
Db     379 KDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPAHLRDAMSAVVGDHNV 438

Qy     427 ICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTK 486
           :|| :   : :  |   : | ||||:| | || |||| |||||||:|||||:   |||
Db     439 VCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDPSLNYTV 498

Qy     487 AEEILSRSIVKRWANFAKYGNPNETQNN-STSWPVFKSTEQKYLTLNTESTRIMTKLRAQ 545
           | | :: ::: | |||: |:||: ::: |  || : :  |:|::|| :   :   ||||
Db     499 EERIFAQRLMQYWTNFARTGDPNDPRDSKSPRWPPYTTAAQQYVSLNLKPLEVRRGLRAQ 558

Qy     546 QCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           | ||  | ||:|  |  :|||| :||| ||||::||: |||||: | ||:| |  |
Db     559 TCAFWNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQERCSDL 614


RESULT 9
ACES_MOUSE
ID   ACES_MOUSE     STANDARD;      PRT;   614 AA.
AC   P21836;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   ACHE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90380429; PubMed=2400605;
RA   Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT   "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT   of alternatively spliced mRNA species.";
RL   Neuron 5:317-327(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=21138439; PubMed=11239002;
RA   Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA   Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA   Miller W., Koop B.F.;
RT   "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT   chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL   Nucleic Acids Res. 29:1352-1365(2001).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX   MEDLINE=96067648; PubMed=8521480;
RA   Bourne Y., Taylor P., Marchot P.;
RT   "Acetylcholinesterase inhibition by fasciculin: crystal structure of
RT   the complex.";
RL   Cell 83:503-512(1995).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=99115643; PubMed=9915834;
RA   Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT   "Crystal structure of mouse acetylcholinesterase. A peripheral site-
RT   occluding loop in a tetrameric assembly.";
RL   J. Biol. Chem. 274:2963-2970(1999).
CC   -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
CC       LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
CC       MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
CC       FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
CC       PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
CC       MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE
CC       ASSOCIATED WITH A SPECIFIC COLLAGEN, COLQ, WHICH TRIGGERS THE
CC       FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY
CC       SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; H AND T (SHOWN HERE); MAY BE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
CC       EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
CC       ACHE PREDOMINATES.
CC   -!- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CC       CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CC       CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
CC       OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
CC       ERYTHROCYTES.
CC   -!- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
CC       SOLUBLE FORM OF ACHE.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56518; CAA39867.1; -.
DR   EMBL; AF312033; AAK28816.1; -.
DR   PIR; JH0314; JH0314.
DR   PDB; 1MAH; 03-APR-96.
DR   PDB; 1MAA; 20-APR-99.
DR   MGD; MGI:87876; Ache.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW   Neurotransmitter degradation; Glycoprotein; Alternative splicing;
KW   3D-structure.
FT   SIGNAL        1     31
FT   CHAIN        32    614       ACETYLCHOLINESTERASE.
FT   ACT_SITE    234    234
FT   ACT_SITE    365    365
FT   ACT_SITE    478    478
FT   DISULFID    100    127
FT   DISULFID    288    303
FT   DISULFID    440    560
FT   DISULFID    611    611       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    296    296       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT   CARBOHYD    381    381       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    495    495       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   614 AA;  68168 MW;  66E2512463C21172 CRC64;

  Query Match           51.9%;  Score 1692.5;  DB 1;  Length 614;
  Best Local Similarity  52.1%;  Pred. No. 4.6e-123;
  Matches  314;  Conservative  106;  Mismatches  172;  Indels   11;  Gaps    5;

Qy      10 IRFLFWFLLLCMLIGKSHTE----DDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPP 65
           :|   |||| :| | :  |      :::  : |::||: |   || |:||||||:|:||
Db      13 LAFPLLFLLLSLLGGGARAEGREDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPP 72

Qy      66 LGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNV 125
           :|  ||  |:    || : :|| : | | | :|  :||| |:|||||| :|||||||||
Db      73 VGSRRFMPPEPKRPWSGVLDATTFQNVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNV 132

Qy     126 WIPAPKPKNAT-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLAL 184
           | | |:| : | |||||||||| :| :|| ||||:|||:||  ::|||||||  |||||
Db     133 WTPYPRPASPTPVLIWIYGGGFYSGAASLDVYDGRFLAQVEGAVLVSMNYRVGTFGFLAL 192

Qy     185 PGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSL 244
           ||: |||||:|| ||:|||||||:|||||||:| ||||||||||||| :|:||  | ||
Db     193 PGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSL 252

Qy     245 FTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEI 300
           | ||:|||| : |||  |  ||| |   ||:| ||    :  |:||:| ||| :  |::
Db     253 FHRAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTELIACLRTRPAQDL 312

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           : :|  |:|  :    :| | ||||||:| |: |:  | |:  |:|||| ||||::|||
Db     313 VDHEWHVLPQESIFRFSFVPVVDGDFLSDTPEALINTGDFQDLQVLVGVVKDEGSYFLVY 372

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           | |||||||  |:|:| :|  |::|  |  |:   |::: |||||:  : | : |:|:  |
Db     373 GVPGFSKDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPTHLRDAMSAV 432

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           |||:| :||  :   : :  |   : | ||||:| | || |||| |||||||:|||||:
Db     433 VGDHNVVCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDP 492

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNN-STSWPVFKSTEQKYLTLNTESTRIM 539
             |||  | | :: ::| | |||: |:||: ::: |  || : :  |:|:::|| :   :
Db     493 SLNYTTEERIFAQRLMKYWTNFARTGDPNDPRDSKSPQWPPYTTAAQQYVSLNLKPLEVR 552

Qy     540 TKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599
           |||| | ||  | ||:|  |  :|||| :||| |||||::||: ||||: | ||:| |
Db     553 RGLRAQTCAFWNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQERC 611

Qy     600 VGL 602
           |
Db     612 SDL 614


RESULT 10
ACES_FELCA
ID   ACES_FELCA     STANDARD;      PRT;   611 AA.
AC   O62763; O62762;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   ACHE.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX   MEDLINE=20334351; PubMed=10874122;
RA   Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA   Lockridge O.;
RT   "Determination of the DNA sequences of acetylcholinesterase and
RT   butyrylcholinesterase from cat and demonstration of the existence of
RT   both in cat plasma.";
RL   Biochem. Pharmacol. 60:479-487(2000).
CC   -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE (BY
CC       SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
CC       LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
CC       MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
CC       FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
CC       PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
CC       MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE
CC       ASSOCIATED WITH A SPECIFIC COLLAGEN, COLQ, WHICH TRIGGERS THE
CC       FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY
CC       SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; H AND T (SHOWN HERE); ARE
CC       PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF053485; AAC08995.1; -.
DR   EMBL; AF053485; AAC08996.1; -.
DR   HSSP; P22303; 2CLJ.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW   Neurotransmitter degradation; Glycoprotein; Alternative splicing.
FT   SIGNAL        1     31       BY SIMILARITY.
FT   CHAIN        32    611       ACETYLCHOLINESTERASE.
FT   ACT_SITE    231    231       BY SIMILARITY.
FT   ACT_SITE    362    362       BY SIMILARITY.
FT   ACT_SITE    475    475       BY SIMILARITY.
FT   DISULFID     97    124       BY SIMILARITY.
FT   DISULFID    285    300       BY SIMILARITY.
FT   DISULFID    437    557       BY SIMILARITY.
FT   DISULFID    608    608       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    293    293       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    378    378       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    492    492       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    572    611       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQDRCSDL
FT                                -> ASKAPSTCSGPAHGEAAPRPRPGLSLPLLLLFLLLSR
FT                                LLR (IN ISOFORM H).
SQ   SEQUENCE   611 AA;  67298 MW;  DFA5C0885A225527 CRC64;

  Query Match           51.6%;  Score 1683;  DB 1;  Length 611;
  Best Local Similarity  51.9%;  Pred. No. 2.5e-122;
  Matches  308;  Conservative  107;  Mismatches  170;  Indels    8;  Gaps    5;

Qy      17 LLLCMLIGKSHTED-DIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQ 75
           ||| :| | :  || :::  : |::||: |   || |:|||||:|:||:|  ||  |:
Db      20 LLLFLLGGGAEAEDPELLVTVRGGQLRGVRLMAPGGPVSAFLGIPFAEPPVGPRRFLPPE 79

Qy      76 SLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNA 135
             |  : :|| : : | | :|  :||| |:|||||| :|||||||||| | |:| :
Db      80 PKRPWPGVLDATAFQSVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPASP 139

Qy     136 T-VLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNM 194
           | ||:|||||| :| ||| ||||:|||: |  ::|||||||| |||||||: |||||:
Db     140 TPVLVWIYGGGFYSGASSLDVYDGRFLAQAEGTVLVSMNYRVGAFGFLALPGSREAPGNV 199

Qy     195 GLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGS 254
           || ||:|||||||| |:| |||:| |||||||||||||| :||||| |  || ||:|||||:
```

```
Db    200 GLLDQRLALQWVQDNVATFGGDPMSVTLFGESAGAASVGMHLLSPPSRGLFHRAVLQSGA 259

Qy    255 FNAPWAVTSLYEARNRTLNLAKLTGC----SRENETEIIKCLRNKDPQEILLNEAFVVPY 310
          | |||   : ||| |   ||:| ||    :  |:||:: ||| :  |::: :|  |:|
Db    260 PNGPWATVGVGEARRRATLLARLVGCPPGGAGGNDTELVACLRTRPAQDLVDHEWHVLPQ 319

Qy    311 GTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNN 370
          :    :| | ||||||:| |: |:  | |   |:|||| |||::|||||||||||||
Db    320 ESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLVGVVKDEGSYFLVYGAPGFSKDNE 379

Qy    371 SIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPA 430
          |:|:| :|  |::: | |:  |::: ||||||:: : |   |||: ||||||:| :||
Db    380 SLISRAQFLAGVRVGVPQASDLAAEAVVLHYTDWLNPEDPARLREAMSDVVGDHNVVCPV 439

Qy    431 LEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEI 490
          :   : :  |   : | ||||:| | || |||| |||||||:||||||   |||  | |
Db    440 AQLAGRLAAQGARVYAYIFEHRASTLSWPLWMGVPHGYEIEFIFGLPLEPSLNYTAEERI 499

Qy    491 LSRSIVKRWANFAKYGNPNETQNNST-SWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRF 549
          :: ::: ||||||: |:||: ::     || : :  |:|::|:     :   |||| | |
Db    500 FAQRLMRYWANFARTGDPNDPRDPKVPQWPPYTAGAQQYVSLDLRPLEVRRGLRAQACAF 559

Qy    550 WTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
          |  | ||:|  |  :|||| :||| ||||::||: ||||||: | ||:: |  |
Db    560 WNRFLPKLLSATDTLDEAERQWKAEFHRWSSYMVHWKNQFDHY-SKQDRCSDL 611


Search completed: January 30, 2003, 11:25:14
Job time : 16 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 30, 2003, 11:24:50 ; Search time 38 Seconds
(without alignments)
3264.220 Million cell updates/sec

Title: US-09-748-739A-2
Perfect score: 3260
Sequence: 1 MDSKVTIICIRFLFWFLLLC.....MDWKNQFNDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2858	87.7	602	6	Q9N1N9	Q9n1n9 equus cabal
2	2784	85.4	602	6	O62760	O62760 felis silve
3	2772	85.0	602	6	O62761	O62761 panthera ti
4	2588	79.4	597	11	Q9JKC1	Q9jkc1 rattus norv
5	2339.5	71.8	603	13	Q90ZK8	Q90zk8 gallus gall
6	1674	51.3	349	6	Q9GKJ6	Q9gkj6 sus scrofa
7	1449	44.4	602	5	O76999	O76999 branchiosto
8	1390	42.6	605	5	O76998	O76998 branchiosto
9	1222.5	37.5	676	5	Q9BMJ1	Q9bmj1 schizaphis
10	1206	37.0	610	5	O97110	O97110 loligo opal
11	1177.5	36.1	677	5	Q9NJH6	Q9njh6 nephotettix
12	1172	36.0	656	5	O96529	O96529 meloidogyne
13	1166	35.8	656	5	Q9XYA9	Q9xya9 meloidogyne
14	1075.5	33.0	637	5	Q9TX11	Q9tx11 aedes aegyp
15	1074.5	33.0	590	5	O61987	O61987 boophilus d
16	1050	32.2	692	5	Q95WV7	Q95wv7 musca domes
17	1050	32.2	692	5	Q95P20	Q95p20 musca domes
18	1047.5	32.1	595	5	O45210	O45210 boophilus m
19	1041.5	31.9	664	5	Q8T7U9	Q8t7u9 myzus persi
20	1033.5	31.7	604	5	Q9NDG8	Q9ndg8 caenorhabdi
21	1029.5	31.6	708	5	P91954	P91954 lucilia cup
22	1025.5	31.5	602	5	O61372	O61372 caenorhabdi
23	1023	31.4	528	5	O62563	O62563 rhipicephal
24	963	29.5	492	5	Q9GQP7	Q9gqp7 apis mellif
25	957.5	29.4	629	5	O61378	O61378 caenorhabdi
26	951	29.2	629	5	O61371	O61371 caenorhabdi
27	945	29.0	604	5	Q9NDG9	Q9ndg9 caenorhabdi
28	937	28.7	607	5	Q9U295	Q9u295 caenorhabdi
29	925	28.4	607	5	O61459	O61459 caenorhabdi
30	873.5	26.8	817	4	Q9ULG0	Q9ulg0 homo sapien
31	858	26.3	836	11	Q62888	Q62888 rattus norv
32	848	26.0	577	5	Q967G8	Q967g8 nippostrong
33	839.5	25.8	582	5	Q9U640	Q9u640 nippostrong
34	838.5	25.7	828	4	Q9NZ94	Q9nz94 homo sapien
35	837	25.7	582	5	O61587	O61587 nippostrong
36	833	25.6	823	4	Q9UPT2	Q9upt2 homo sapien
37	832	25.5	848	11	Q62889	Q62889 rattus norv
38	831.5	25.5	828	4	Q9NZ97	Q9nz97 homo sapien
39	831.5	25.5	848	4	Q9NZ95	Q9nz95 homo sapien
40	826.5	25.4	560	11	Q8R097	Q8r097 mus musculu
41	818	25.1	540	5	Q9GPL0	Q9gpl0 dictyocaulu
42	814	25.0	843	11	Q62765	Q62765 rattus norv
43	792	24.3	558	11	Q8QZR3	Q8qzr3 mus musculu
44	788.5	24.2	559	11	O35533	O35533 mesocricetu
45	776	23.8	561	11	Q91WG0	Q91wg0 mus musculu

ALIGNMENTS

RESULT 1
Q9N1N9
ID Q9N1N9 PRELIMINARY; PRT; 602 AA.
AC Q9N1N9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Butyrylcholinesterase (EC 3.1.1.8).
GN BCHE.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20181263; PubMed=10718335;
RA Wierdl M., Morton C.L., Danks M.K., Potter P.M.;
RT "Isolation and characterization of a cDNA encoding a horse liver
RT butyrylcholinesterase: Evidence for CPT-11 drug activation.";
RL Biochem. Pharmacol. 59:773-781(2000).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF178685; AAF61480.1; -.
DR HSSP; P21836; 1MAH.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; COesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 602 AA; 68838 MW; 94C73F00431DF26E CRC64;

Query Match 87.7%; Score 2858; DB 6; Length 602;
Best Local Similarity 89.6%; Pred. No. 2.4e-217;
Matches 537; Conservative 20; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60

```
Db      1 MQSWGTIICIRILLRFLLLWVLIGNSHTEEDIIITTKNGKVRGMNLPVLGGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
          ||||||||||||||||||||:||||||||||| || ||||||| |||||||||:|||||
Db     61 YAQPPLGRLRFKKPQSLTKWSNIWNATKYANSCYQNTDQSFPGFLGSEMWNPNTELSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          ||||||||||||||||:|||||||||||||| ||||||||||||||||||||||||||||
Db    121 LYLNVWIPAPKPKNATVMIWIYGGGFQTGTSSLPVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          ||||  ||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db    181 FLALSENPEAPGNMGLFDQQLALQWVQKNIAAFGGNPRSVTLFGESAGAASVSLHLLSPR 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          |  ||||||||||| |||||||||||||||||| |||  ||||:||||:||||||:||||||
Db    241 SQPLFTRAILQSGSSNAPWAVTSLYEARNRTLTLAKRMGCSRDNETEMIKCLRDKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          |||| |||||  | ||||||||||||||||||| ||:|||||:|||||||||||||| ||||
Db    301 LLNEVFVVPYDTLLSVNFGPTVDGDFLTDMPDTLLQLGQFKRTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          |||||||||||||||||||||||||| |||||:||||||| ||:|||| ||||||| ||
Db    361 GAPGFSKDNNSIITRKEFQEGLKIFFPRVSEFGRESILFHYMDWLDDQRAENYREALDDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
          ||||| |||||||||||| ||:|||||||||:|||||||||||||||||||||||||||||
Db    421 VGDYNIICPALEFTKKFSELGNDAFFYYFEHRSTKLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          | ||||||||||||:||||||||||||| ||:||| |||||||||||||||||| :: |
Db    481 RVNYTKAEEILSRSIMKRWANFAKYGNPNGTQSNSTRWPVFKSTEQKYLTLNTESPKVYT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599
          |||||||||||  |||||||:|||||||| ||||||||||||||||||||||||||||||
Db    541 KLRAQQCRFWTLFFPKVLELTGNIDEAEREWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599


RESULT 2
O62760
ID   O62760      PRELIMINARY;      PRT;   602 AA.
AC   O62760;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   CHOLINESTERASE precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (Pseudocholinesterase)
DE   (BUTYRYLCHOLINESTERASE).
GN   BCHE.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE=20334351; PubMed=10874122;
RA   Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA   Lockridge O.;
RT   "Determination of the DNA sequences of acetylcholinesterase and
RT   butyrylcholinesterase from cat and demonstration of the existence of
RT   both in cat plasma.";
RL   Biochem. Pharmacol. 60:479-487(2000).
CC   -!- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H(2)O = CHOLINE + A
CC       CARBOXYLIC ACID ANION.
CC   -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC       TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND (BY
CC       SIMILARITY).
CC   -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC       ORGANOPHOSPHATE ESTERS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AF053483; AAC06261.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Glycoprotein; Signal.
FT   SIGNAL       1     28       POTENTIAL.
FT   CHAIN       29    602       BUTYRYLCHOLINESTERASE.
FT   ACT_SITE    226   226       BY SIMILARITY.
FT   ACT_SITE    353   353       BY SIMILARITY.
FT   ACT_SITE    466   466       BY SIMILARITY.
FT   DISULFID     93   120       BY SIMILARITY.
FT   DISULFID    280   291       BY SIMILARITY.
FT   DISULFID    428   547       BY SIMILARITY.
FT   DISULFID    599   599       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     85    85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134   134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    269   269       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284   284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    369   369       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    483   483       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    509   509       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    513   513       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    514   514       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   602 AA;  68328 MW;  ECB8879232B74B9C CRC64;

  Query Match           85.4%;  Score 2784;  DB 6;  Length 602;
  Best Local Similarity 86.9%;  Pred. No. 1.7e-211;
  Matches  523;  Conservative   24;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
          | || ||| |:|| |||| :||||||:|||| |||||||||| | |||||||||
Db      1 MQSKGTIISIQFLLRFLLLWVLIGKSHTEEDIIITTKNGKVRGMNLPVLDGTVTAFLGIP 60

Qy     61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCYQNADQSFPGFPGSEMWNPNTDLSEDC 120
          |||||||||||||| |||||||||||||||| || ||||||| ||||||||||||||
Db     61 YAQPPLGRLRFKKPQFLTKWSDIWNATKYANSCYQNADQSFPGFPGSEMWNPNTDLSEDC 120

Qy    121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
          |||||||| |||||||:|||||||||||||| ||||||||||||||||||||||||||||
Db    121 LYLNVWIPTPKPKNATVMIWIYGGGFQTGTSSLPVYDGKFLARVERVIVVSMNYRVGALG 180

Qy    181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
          |||||||| |||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    181 FLALPGNPEVPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAGSVSLHLLSPR 240

Qy    241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
          |  |||||||||| |||||| || ||:|||| |||  |||:|||:||||||||||||||||
Db    241 SQPLFTRAILQSGSSNAPWAVMSLDEAKNRTLTLAKFIGCSKENDTEIIKCLRNKDPQEI 300

Qy    301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
          ||||  |||  | ||||||| |||||||||| ||:|||||||||||||||||| ||||
Db    301 LLNELLVVPSDTLLSVNFGPVVDGDFLTDMPDTLLQLGQFKKTQILVGVNKDEGTAFLVY 360

Qy    361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
          |||||||||:|||||||||||||||:||||||:|:|||:| | :|||| | ||||||
Db    361 GAPGFSKDNDSIITRKEFQEGLKIYFPGVSEFGREAILFYYVDLLDDQRAEKYREALDDV 420

Qy    421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
          :|||| |||||||| |||| |||||||||||||:|||||||||||||||||||||||||||
Db    421 LGDYNIICPALEFTTKFSELGNNAFFYYFEHRSSQLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy    481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
          | |||:|||||||||:  |||||||||| |||||| || |:||:|||||| || :: |
Db    481 RVNYTRAEEILSRSIMNYWANFAKYGNPNGTQNNSTRWPAFRSTDQKYLTLNAESPKVYT 540

Qy    541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
          |||||||||| |||||||||||||||| ||:|||:||||||||||||||||||||||||||
Db    541 KLRAQQCRFWTLFFPKVLEMTGNIDEAEREWRAGFYRWNNYMMDWKNQFNDYTSKKESCA 600
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Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 3
O62761
ID   O62761      PRELIMINARY;      PRT;   602 AA.
AC   O62761;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   CHOLINESTERASE precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (Pseudocholinesterase)
DE   (BUTYRYLCHOLINESTERASE).
GN   BCHE.
OS   Panthera tigris tigris (Bengal tiger).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
OX   NCBI_TaxID=74535;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PITUITARY;
RX   MEDLINE=20334351; PubMed=10874122;
RA   Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA   Lockridge O.;
RT   "Determination of the DNA sequences of acetylcholinesterase and
RT   butyrylcholinesterase from cat and demonstration of the existence of
RT   both in cat plasma.";
RL   Biochem. Pharmacol. 60:479-487(2000).
CC   -!- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H(2)O = CHOLINE + A
CC       CARBOXYLIC ACID ANION.
CC   -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC       TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND (BY
CC       SIMILARITY).
CC   -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC       ORGANOPHOSPHATE ESTERS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AF053484; AAC06262.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Serine esterase; Glycoprotein; Signal.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    602       BUTYRYLCHOLINESTERASE.
FT   ACT_SITE    226    226       BY SIMILARITY.
FT   ACT_SITE    353    353       BY SIMILARITY.
FT   ACT_SITE    466    466       BY SIMILARITY.
FT   DISULFID     93    120       BY SIMILARITY.
FT   DISULFID    280    291       BY SIMILARITY.
FT   DISULFID    428    547       BY SIMILARITY.
FT   DISULFID    599    599       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    269    269       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    369    369       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    483    483       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    509    509       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    513    513       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    514    514       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   602 AA;  68289 MW;  EB0C8B9148E956A1 CRC64;

  Query Match             85.0%;  Score 2772;  DB 6;  Length 602;
  Best Local Similarity   86.5%;  Pred. No. 1.5e-210;
  Matches  521;  Conservative   25;  Mismatches   56;  Indels    0;  Gaps    0;

Qy       1 MDSKVTIICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
           | || ||| |:|| |||| :||||||||:|||| |||||||||| |  ||||||||||
Db       1 MQSKGTIISIQFLLRFLLLWVLIGKSHTEEDIIITTKNGKVRGMNLPVLDGTVTAFLGIP 60

Qy      61 YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDC 120
           ||||||||||||||| ||||||||||||:|||| || ||||||| ||||||||||||||
Db      61 YAQPPLGRLRFKKPQFLTKWSDIWNATKHANSCYQNADQSFPGFPGSEMWNPNTDLSEDC 120

Qy     121 LYLNVWIPAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALG 180
           |||||| | ||||||||:|||||||||||||||| ||||||||||||||||||||||||||
Db     121 LYLNVWSPTPKPKNATVMIWIYGGGFQTGTSSLPVYDGKFLARVERVIVVSMNYRVGALG 180

Qy     181 FLALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPG 240
           |||||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     181 FLALPGNPEIPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAGSVSLHLLSPR 240

Qy     241 SHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEI 300
           |  |||||||||| |||||| || ||:|||| ||| |||:||:|||||||||||||||
Db     241 SQPLFTRAILQSGSSNAPWAVMSLDEAKNRTLTLAKFIGCSKENDTEIIKCLRNKDPQEI 300

Qy     301 LLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVY 360
           |.||| ||| | |||||| |||||||||| ||:||||||||||||||||| ||||
Db     301 LLNELLVVPSDTLLSVNFGPVVDGDFLTDMPDTLLQLGQFKKTQILVGVNKDEGTAFLVY 360

Qy     361 GAPGFSKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
           |||||||||:|||||||||||||:||||||||:|:|||:| | :|||| | ||||| ||
Db     361 GAPGFSKDNDSIITRKEFQEGLKIYFPGVSEFGREAILFYYVDLLDDQRAEKYREALDDV 420

Qy     421 VGDYNFICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLER 480
           :|||| |||||||| |||| ||||||||||||||:|||||||||||||||||||||||||
Db     421 LGDYNIICPALEFTTKFSELGNNAFFYYFEHRSSQLPWPEWMGVMHGYEIEFVFGLPLER 480

Qy     481 RDNYTKAEEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMT 540
           | |||:||||||||:  |||||||||| |||||| || |:|||:||||||| || ;: |
Db     481 RVNYTRAEEILSRSIMNYWANFAKYGNPNGTQNNSTRWPAFRSTDQKYLTLNAESPKVYT 540

Qy     541 KLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCV 600
           |||||||||| |||||||||||||| ||:|||:|||||||||||||||||||||||||||
Db     541 KLRAQQCRFWTLFFPKVLEMTGNIDEAEREWRAGFYRWNNYMMDWKNQFNDYTSKKESCA 600

Qy     601 GL 602
           ||
Db     601 GL 602


RESULT 4
Q9JKC1
ID   Q9JKC1      PRELIMINARY;      PRT;   597 AA.
AC   Q9JKC1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Butyrylcholinesterase.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Li B., Stribley J., Ticu A., Xie W., Schopfer L.M., Hammond P.,
RA   Brimijoin S., Hinrichs S.H., Lockridge O.;
RT   "Abundant Tissue Butyrylcholinesterase and its Possible Function in
RT   the Acetylcholinesterase Knockout Mouse.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AF244349; AAF44713.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
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DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
SQ   SEQUENCE   597 AA;  67776 MW;  771204D166C7EEAC CRC64;

  Query Match             79.4%;  Score 2588;  DB 11;  Length 597;
  Best Local Similarity   79.8%;  Pred. No. 5.3e-196;
  Matches  473;  Conservative   47;  Mismatches   73;  Indels    0;  Gaps    0;

Qy      10 IRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRL 69
           | || | |||||| ||||||:|:|| || |:|||::: : |||||||||||||||||| |
Db       5 IHFLLWILLLCMLFGKSHTEEDVIITTKTGRVRGLSMPILGGTVTAFLGIPYAQPPLGSL 64

Qy      70 RFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPA 129
           |||||| | || |::|||||||||.|||||:|||| |||||||||:|||||||||||||
Db      65 RFKKPQPLNKWPDVYNATKYANSCYQNIDQAFPGFQGSEMWNPNTNLSEDCLYLNVWIPV 124

Qy     130 PKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPE 189
           |||||||||::|:|||||||||||||| ||||||| ||||||||||||||||||||| ||| |
Db     125 PKPKNATVMVWVYGGGFQTGTSSLPVYDGKFLTRVERVIVVSMNYRVGALGFLAFPGNSE 184

Qy     190 APGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAI 249
           |||||||||||||||:|:|||||||||||||||||||||||||||||| | |: ||||||
Db     185 APGNMGLFDQQLALQWIQRNIAAFGGNPKSVTLFGESAGAASVSLHLLCPQSYPLFTRAI 244

Qy     250 LQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVP 309
           |:|:| ||||||    |||||| ||| |||:||| ||| |||:|||||||||  |:|
Db     245 LESGSSNAPWAVKHPEEARNRTLTLAKFIGCSKENEKEIITCLRSKDPQEILLNEKLVLP 304

Qy     310 YGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDN 369
             :  |:|||||||||||||||  ||:||: |  |||||||||||| ||||||||||||
Db     305 SDSIRSINFGPTVDGDFLTDMPHTLLQLGKVKTAQILVGVNKDEGTAFLVYGAPGFSKDN 364

Qy     370 NSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICP 429
           :|:|||:|||||| ::|||||  |||:|||:| ||: || || |||  |::|||| |||
Db     365 DSLITRREFQEGLNMYFPGVSSLGKEAILFYYVDWLGDQTPEVYREAFDDIIGDYNIICP 424

Qy     430 ALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEE 489
           ||||||||:|  ||||||||||||||||||||||||||||||||||||||| |||:|||
Db     425 ALEFTKKFAELEINAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRVNYTRAEE 484

Qy     490 ILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRF 549
           | ||||:| |||||||||:|| || ||| |||| |||||||||||| ::| :|||| ||:|
Db     485 IFSRSIMKTWANFAKYGHPNGTQGNSTVWPVFTSTEQKYLTLNTEKSKINSKLRAPQCQF 544

Qy     550 WTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVGL 602
           |  |||||||:||:||| | |||||||||:|||||||||||||||||:|  |
Db     545 WRLFFPKVLEITGDIDEREQEWKAGFHRWSNYMMDWKNQFNDYTSKKETCTDL 597


RESULT 5
Q90ZK8
ID   Q90ZK8      PRELIMINARY;      PRT;   603 AA.
AC   Q90ZK8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Butyrylcholinesterase precursor (EC 3.1.1.8).
GN   BCHE.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Geissler K., Chatonnet A., Layer P.G.;
RT   "Chicken Butyrylcholinesterase.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AJ306928; CAC37792.1; -.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; UNKNOWN_1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; UNKNOWN_1.
KW   Hydrolase; Signal.
FT   SIGNAL       1     29       POTENTIAL.
FT   CHAIN       30    603       BUTYRYLCHOLINESTERASE.
SQ   SEQUENCE   603 AA;  68480 MW;  A350FDDF68574ADF CRC64;

  Query Match             71.8%;  Score 2339.5;  DB 13;  Length 603;
  Best Local Similarity   71.9%;  Pred. No. 2.4e-176;
  Matches  427;  Conservative   70;  Mismatches   96;  Indels    1;  Gaps    1;

Qy       8 ICIRFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLG 67
           || ||| | ||| | | |   ||: :| |: |:||| || | ||||||||||| :||:|
Db       9 ICARFLMWLLLLFMFIRKVVPEDN-VITTEKGRVRGTNLQVLGGTVTAFLGIPYGKPPIG 67

Qy      68 RLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWI 127
           ||||:||:   ||| || |||:|||| | || ::||| |:|||||  |:||||||||||||
Db      68 RLRFQKPEPFEKWSGIWKATKHANSCYQLIDTTYPGFPGTEMWNPKTNLSEDCLYLNVWI 127

Qy     128 PAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGN 187
           |:|||||||::|||||  |:||::|| |||||||||||||||||||| ||||||||||
Db     128 PSPKPKNATVMVWIYGGSFETGSTSLPVYDGKFLARVERVIVVSMNYRTGALGFLALPGN 187

Qy     188 PEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTR 247
           | ||| ||||||:|||||||:|||:|||||||||:||||||:|||| |:||| || ||||
Db     188 KEVPGNAGLFDQRLALQWVQENIASFGGNPKSVTIFGESAGSASVSYHILSPKSHPLFTR 247

Qy     248 AILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFV 307
           ||:|||| |||||  :  ||| ||: |||   |   :|||:| ||::|||::|| || :|
Db     248 AIMQSGSANAPWAAITASEARRRTVALAKQLKCPTSDETELILCLQDKDPKDILENEVYV 307

Qy     308 VPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSK 367
           | | : | : | |||||||| |||: |:: | ||:||:|||||||||| ||||| |||||
Db     308 VKYFSLLHIYFCPTVDGDFLADMPEALIKNGIFKQTQVLVGVNKDEGTSFLVYGVPGFSK 367

Qy     368 DNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFI 427
           |::|:| : :|:  | : || ||:  |||:| |||| ::|:||:||:|: ||:|||: |
Db     368 DSDSLINKTQFEVALTLSFPQVSKLAIESIIFQYTDWENEQKPEHYRDAMDDVIGDYHII 427

Qy     428 CPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKA 487
           |||:|| |  :| ||| |||:|||||||||||||||||||||||||||||||| ||||
Db     428 CPAVEFAKTIAEVGNNVFFYFFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRVNYTKA 487

Qy     488 EEILSRSIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQC 547
           |||||||::: ||:||| |||| |  | | |||| ||||||||||::: |:||||||||
Db     488 EEILSRSMLRYWASFAKTGNPNGTLINGTRWPVFTSTEQKYLTLNTDASEILTKLRAQQC 547

Qy     548 RFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESCVG 601
           |||  |||||||||||||||| ||||||||||||||||||||||||||| | |
Db     548 RFWNMFFPKVLEMTGNIDEAEREWKAGFHRWNNYMMDWKNQFNDYTSKKERCAG 601


RESULT 6
Q9GKJ6
ID   Q9GKJ6      PRELIMINARY;      PRT;   349 AA.
AC   Q9GKJ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Butyrylcholinesterase (Fragment).
GN   BCHE.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van Poucke M., Yerle M., Tuggle C., Chardon P., Van Zeveren A.,
RA   Peelman L.J.;
RT   "Integration of porcine chromosome 13 maps.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AF222914; AAG41127.1; -.
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DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
KW   Hydrolase.
FT   NON_TER       1      1
FT   NON_TER     349    349
SQ   SEQUENCE   349 AA;  39061 MW;  D66354B14725BE58 CRC64;

  Query Match           51.3%;  Score 1674;  DB 6;  Length 349;
  Best Local Similarity   91.4%;  Pred. No. 4.3e-124;
  Matches  319;  Conservative    6;  Mismatches   24;  Indels    0;  Gaps    0;

Qy     141 IYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQ 200
           ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1 IYGGGFQTGTSSLHVYDGKFLSRVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQQ 60

Qy     201 LALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWA 260
           |||||||||||||||||||||||||||| ||||||||| || || |||||||| |||||
Db      61 LALQWVQKNIAAFGGNPKSVTLFGESAGAVSVSLHLLSPRSHPLFARAILQSGSSNAPWA 120

Qy     261 VTSLYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGP 320
           ||||||||||| |||  |||||||||||||||||||||||| || ||||    |||||||
Db     121 VTSLYEARNRTLTLAKFIGCSRENETEIIKCLRNKDPQEILQNEVFVVPNHMLLSVNFGP 180

Qy     321 TVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFSKDNNSIITRKEFQE 380
           |||||||||:|| ||:|||||||||||||||||| | ||||||||||||||||||||:|
Db     181 TVDGDFLTDLPDTLLQLGQFKKTQILVGVNKDEGTAFSVYGAPGFSKDNNSIITRKEFEE 240

Qy     381 GLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEW 440
           |||||||||||||||||||| || |||| ||||:|| ||||||: ||||||||||||||
Db     241 GLKIFFPGVSEFGKESILFHYMDWTDDQRAENYRDALDDVVGDYDIICPALEFTKKFSEM 300

Qy     441 GNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEE 489
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     301 GNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRANYTKAEE 349


RESULT 7
O76999
ID   O76999      PRELIMINARY;      PRT;   602 AA.
AC   O76999;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cholinesterase 2 (EC 3.1.1.7).
GN   CHE2.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99089603; PubMed=9874207;
RA   McClellan J.S., Coblentz W.B., Sapp M., Rulewicz G., Gaines D.I.,
RA   Hawkins A., Ozment C., Bearden A., Merritt S., Cunningham J.,
RA   Palmer E., Contractor A., Pezzementi L.;
RT   "cDNA cloning, in vitro expression, and biochemical characterization
RT   of cholinesterase 1 and cholinesterase 2 from amphioxus--comparison
RT   with cholinesterase 1 and cholinesterase 2 produced in vivo.";
RL   Eur. J. Biochem. 258:419-429(1998).
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; U74381; AAD05374.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
SQ   SEQUENCE   602 AA;  66491 MW;  1D29ABF76618C2EE CRC64;

  Query Match           44.4%;  Score 1449;  DB 5;  Length 602;
  Best Local Similarity   46.3%;  Pred. No. 6.1e-106;
  Matches  276;  Conservative  104;  Mismatches  174;  Indels   42;  Gaps    7;

Qy      14 FWFLLLCMLI------GKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLG 67
           :|| :| : :       :: | :  |: |  |:::|  | | | || |||||||  ||:|
Db       7 YWFFVLLVNLTAHTWTAEAQTTNGPIVTTLQGRLQGKVLDVGGRTVNAFLGIPYGAPPVG 66

Qy      68 RLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWI 127
            ||| | :   |: |:||: | |:| |  | :|||: |:|||||||| :||||||||||
Db      67 PRRFKPPIAAEPWNGIYNASSYPNTCMQLPDTTFPGYKGAEMWNPNTPVSEDCLYLNVWQ 126

Qy     128 PAPKPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGN 187
           |:| |  |||::||||||| :||||| ||||::||| : ||| ||||| ||:|||:| ||
Db     127 PSPVPVGATVMVWIYGGGFMSGTSSLDVYDGRYLARTQGVIVASMNYRTGAMGFLSL-GN 185

Qy     188 PEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTR 247
           |||||:|| || ||| |:::|:|:||| |  |::|||||||||| ||||| | :|| |
Db     186 SEAPGNVGLMDQNLALTWIKENVASFGGAPNKVSIFGESAGAASVSYHLLSPMSKNLFQR 245

Qy     248 AILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENE-TEIIKCLRNKDPQEILLNEAF 306
           ||::| |  :|||: |  ||  | : | |  ||| :::  | |:|:|    | |  ||
Db     246 AIMESASAPSPWALLSDTEAYRRGIELPKAVGCSTDSDLEETIECMRGVPAQTISDNEWV 305

Qy     307 VVPYGTPLSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGFS 366
           |  :|      | | |||:|: : |   |: |  |:| :||| | ||| :||:|||||||
Db     306 V--WGL-CQFPFAPIVDGNFIREHPTQSLQTGNLKQTDVLVGFNNDEGVYFLLYGAPGFS 362

Qy     367 KDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNF 426
           ||  |:|||::: ||:|:   |:::   ::: | | ||||  :|  ||:|: |: |||||
Db     363 KDTRSLITREQYLEGIKMSVMGINDISVDALSFQYIDWVNFDQPSMYRDAIDDLSGDYNF 422

Qy     427 ICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTK 486
           ||||| | |  :  |   : | | |::| :|||:| ||||||| ||||||| ::::|||:
Db     423 ICPALSFGKAMASLGRKTYQYKFVHQASNMPWPKWTGVMHGYECEFVFGLPTDQKNNYTQ 482

Qy     487 AEEILSRSIVKRWANFAKYGNPNETQNNSTS---WPVFKSTEQKYLTLNTESTRIMTKLR 543
           | : :  |: |||||| ||||:      :  |  :    |:|| |:     |    |
Db     483 EEAVFATQIMTYWANFAKTGNPNKQTLEDPAPDVWRPYTDEGQEYLILDVGGNRMANGPR 542

Qy     544 AQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQFNDYTSKKESC 599
           :: | |                              |:||: :   : :|   : :||
Db     543 SKSCAF----------------------------WDNYLWELDRKTDDLMEQAQSC 570


RESULT 8
O76998
ID   O76998      PRELIMINARY;      PRT;   605 AA.
AC   O76998;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cholinesterase 1 (EC 3.1.1.7).
GN   CHE1.
OS   Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99089603; PubMed=9874207;
RA   McClellan J.S., Coblentz W.B., Sapp M., Rulewicz G., Gaines D.I.,
RA   Hawkins A., Ozment C., Bearden A., Merritt S., Cunningham J.,
RA   Palmer E., Contractor A., Pezzementi L.;
RT   "cDNA cloning, in vitro expression, and biochemical characterization
RT   of cholinesterase 1 and cholinesterase 2 from amphioxus--comparison
RT   with cholinesterase 1 and cholinesterase 2 produced in vivo.";
RL   Eur. J. Biochem. 258:419-429(1998).
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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DR   EMBL; U74380; AAD05373.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
SQ   SEQUENCE   605 AA;  67300 MW;  E102ED7A2DC80688 CRC64;

  Query Match             42.6%;  Score 1390;  DB 5;  Length 605;
  Best Local Similarity   48.0%;  Pred. No. 2.9e-101;
  Matches  278;  Conservative   94;  Mismatches  195;  Indels   12;  Gaps    7;

Qy      11 RFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLR 70
           | |   | | ||:  |        :: |  |:|||: | | |   | |||||||:|:||:|.||
Db       4 RLLLQILPLLMLVRTSVDAATSVVQTSAGQVRGLELDVLGRKVNAFLGIPFAKPPVGDLR 63

Qy      71 FKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAP 130
           |: |:    |: :::||:: |||    |::|||||:|||||| :|||||||||| | |
Db      64 FRAPEPADSWT-LYDATQFPNSCVSAPDEAFPGFHGAEMWNPNTPISEDCLYLNVWQPTP 122

Qy     131 KPKNATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEA 190
             | ||||:||||||| :||||| ||||::|||:| |:||||||:||||||   |:  |
Db     123 APTGATVLVWIYGGGFFSGTSSLDVYDGRYLARMEDVVVVSMNYRLGALGFL-YSGSEAA 181

Qy     191 PGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAIL 250
           |||:|| || ||| |||:|: ||||:|  ||:|||||||||||: |:|| | :|| |||:
Db     182 PGNVGLLDQHLALLWVQQNVHAFGGDPAKVTIFGESAGAASVNFHMISPMSRNLFQRAIM 241

Qy     251 QSGGSFNAPWAVTSLYEARNRTLNLAKLTGCSRENE--TEIIKCLRNKDPQEILLNEAFVV 308
           || |  ||||:    :|| ||  ||   ||| | |    :: |||:   | || :|  ||
Db     242 QSASALAPWALRPSEQARKRTKALAIDIGCSAEEEDMDALVACLRDVPAQTILDHEWNVV 301

Qy     309 PYGTP---LSVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPGF 365
                 : | |  || |||: |  : | | ||   ||||  |:|| ::|||| |||
Db     302 DLTGAHFLADIPFPPPIKDGSFLTEDPTEVYEKGTFKDIDILVGFVKNEGNFWLVYGVPGF 361

Qy     366 SKDNNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYN 425
           ||| :||| |  |   ::   | :::   |:  | ||||:   :   ||:||  | |||
Db     362 SKDTDSIIDRDTFVGDIEFCHPWLNDITVEATAFEYTDWLHMDQDTMYRDALDSVFGDYF 421

Qy     426 FICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYT 485
           |:||     |   | : | |   :| | || ||| |||||||:||||:: : |||
Db     422 FVCPTTAVGKGHVNHGRTAYVYEFAQVASNLAWPHWMGAMHGYEIEFIFGLPIDPKWNYT 481

Qy     486 KAEEILSRSIVKRWANFAKYGNPNETQNNSTS---WPVFKSTEQKYLTLNTESTRIMTKL 542
             |  |:| ::: | |||: ||||:   : |:   |  :    ::|: |:|: ||::
Db     482 AEEGELARRMMRYWTNFARTGNPNKRSPDDTTDDIWRPYTEEGREYIILDTDGTRMLNGP 541

Qy     543 RAQQCRFWTSFFPKVLEMTGN-IDEAEWEWKAGFHRWNN 580
           :::|| ||  : | : : | : |::||    :|   | :
Db     542 KSKQCAFWERYMPSLQKETDDLINDAE-PCSSGGRSWRS 579


RESULT 9
Q9BMJ1
ID   Q9BMJ1      PRELIMINARY;      PRT;   676 AA.
AC   Q9BMJ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Acetylcholinesterase (EC 3.1.1.7).
OS   Schizaphis graminum (Aphid).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
OC   Aphidiformes; Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX   NCBI_TaxID=13262;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gao J.R., Zhu K.Y.;
RT   "Cloning, sequencing and phylogenetic analysis of an
RT   acetylcholinesterase gene from the greenbug, Schizaphis graminum
RT   (Homoptera: Aphididae).";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AF321574; AAK09373.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; UNKNOWN_1.
KW   Hydrolase.
SQ   SEQUENCE   676 AA;  76451 MW;  9F8DBBAE5E7D5CE1 CRC64;

  Query Match             37.5%;  Score 1222.5;  DB 5;  Length 676;
  Best Local Similarity   46.0%;  Pred. No. 6e-88;
  Matches  250;  Conservative   81;  Mismatches  195;  Indels   17;  Gaps    8;

Qy      26 SHTEDD-IIIATKNGKVRGMNLT-VFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKW--- 80
           ::| || :|| |  ||:||:  |    |  | |:|||||: |:| |||: |: : :|
Db      95 AYTSDDPLIIHTNKGKIRGITQTATTGKLVDAWLGIPYAKKPIGDLRFRHPRPIDRWDTT 154

Qy      81 --SDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPKNATVL 138
               | |   |:| |  |  |  | |: |||||: :||||||:|| :| |:|:|| |:
Db     155 TPETILNCTTPPNTCVQIFDTLFGDFPGATMWNPNSPVSEDCLYINVVVPKPRPQNAAVM 214

Qy     139 IWIYGGGFQTGTSSLHVYDGKFLARVERYIVVSMNYRVGALGFLALPGNPEAPGNMGLFD 198
           :||:|||| :|:::| :|| | |   | ||:||| ||| :|||      : ||| ||||
Db     215 VWIFGGGFYSGSATLDIYDPKILVSEENVILVSMQYRVASLGFLYF-DTEDVPGNAGLFD 273

Qy     199 QQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
           | :|||||| :|| ||||| :|||||||||| |||||||||  | :|| :||::|||  ||
Db     274 QLMALQWVHENIKLFGGNPNNVTLFGESAGAVSVSLHLLSPLSRNLFNQAIMESGSSTAP 333

Qy     259 WAVTSLYEARNRTLNLAKLTGCSRENET--EIIKCLRNKDPQEILLNEAFVVPYGTPLSV 316
           ||: |  |: || | |||  ||  :  |  : ::|||  :   ::  |   |
Db     334 WAILSREESFNRGLKLAKAMGCPDDRNTIHKTVECLRKANSSVMVEKEWDHVAI---CFF 390

Qy     317 NFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPG-FSKDNNSIITR 375
           | | ||| || | |   |    |||| ||:| | :|| : : |      | |: | :::|
Db     391 PFVPVVDGAFLDDHPQKSLSTNNFKKTNILMGSNSEEGYYSIFYYLTELFKKEENVMVSR 450

Qy     376 KEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTK 435
           : | : :      |      | :| | ||||     ||  | ||  ||||  | |   ||
Db     451 ENFIKAIGQLNPNADAAVKSAIEFEYTDWFSPNDPEKNRNALDKMVGDYQFTCNVNEFAH 510

Qy     436 KFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSRSI 495
           |::  ||| : |||:|||   |||:| ||||| || :||| ||      |   |  ||: :
Db     511 KYALTGNNVYMYYFKHRSLNNPWPKWTGVMHGDEISYVFGDPLNPNKRYEIEEIELSKKM 570

Qy     496 VKRWANFAKYGNPNETQNNS---TSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTS 552
           :: | |||| |||::|    |     |||  :  :::|||:| :| |    | :|| || :
Db     571 MRYWTNFAKTGNPSKTLEGSWVTPKWPVHTAYGKEFLTLDTNNTSIGVGPRLEQCAFWKN 630

Qy     553 FFP 555
           : |
Db     631 YVP 633


RESULT 10
O97110
ID   O97110      PRELIMINARY;      PRT;   610 AA.
AC   O97110;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Acetylcholinesterase (Fragment).
OS   Loligo opalescens (California market squid).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
OC   Myopsida; Loliginidae; Loligo.
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OX   NCBI_TaxID=31211;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OPTIC LOBE;
RA   Talesa V., Grauso M., Arpagaus M., Giovannini E., Romani R., Rosi G.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR   EMBL; AF065384; AAD15886.1; -.
DR   HSSP; P21836; 1MAA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs_site.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
FT   NON_TER     610    610
SQ   SEQUENCE   610 AA;  69516 MW;  53EB4FFE11112063 CRC64;

  Query Match             37.0%;  Score 1206;  DB 5;  Length 610;
  Best Local Similarity   43.1%;  Pred. No. 1e-86;
  Matches  245;  Conservative  101;  Mismatches  198;  Indels   24;  Gaps   10;

Qy      18 LLCMLIGKSHTEDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSL 77
           :||: :       | ||:|  |||||: : |:   | |||||||:|:||:| |||: |
Db      17 ILCLFVLAEAYNSDPIISTSKGKVRGLRINVYDKQVDAFLGIPFAKPPVGNLRFRHPVPN 76

Qy      78 TKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPA--PKPKNA 135
             |: |::||:  ||| |  |: |  | |  ||: || ||||||||||:|      |
Db      77 DPWTGIYDATRKPNSCIQGFDRIFTNFSGETMWHANTQLSEDCLYLNVWVPRNDKSKKKK 136

Qy     136 TVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMG 195
           |::|||||||| :|||:| ||| : |     :| ||| ||| | ||||| | |||||| |
Db     137 AVMVWIYGGGFYSGTSTLDVYDPRHLVAENDIIFVSMQYRVSAFGFLAL-GIPEAPGNAG 195

Qy     196 LFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSF 255
           :||| :|| |||:||  |||||::|||||||||||||: ||||| |   | ||||||||
Db     196 MFDQLMALDWVQRNIKFFGGNPQNVTLFGESAGAASVAFHLLSPLSRPKFDRAILQSGSV 255

Qy     256 NAPWAVTSLYEARNRTLNLAKLTGCS-RENETEIIKCLRNKDPQEILLNEAFVVPYGTPL 314
             ||||:  ||  |   ||:   |   :   :: :||: :   |   :| :|:   :
Db     256 TCAWAVTTREEAFRRAKTLARQFKCPVLDTAMDVYQCLKAQPADEFPDHEWWVIQGISQF 315

Qy     315 SVNFGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTWFLVYGAPG-FSKDNNSII 373
             |   ||| || : |:| ||   |||  |||| ||:|||:|| |     |:  ::::|
Db     316 P--FVLVVDGTFLVEAPEIALERHAFKKVPILVGTNKNEGTYFLTYFRQDIFNLKDSALI 373

Qy     374 TRKEFQ---EGLKIFFP----GVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDYNF 426
           ::  |:   : |  ::|     :: ||:::||: || | |     : |  :  :| ||:|
Db     374 SKSIFRLLLDTLVEYYPKYPHSLNSFGRDAILYQYTHWADPDDMLHNRNMIDQLVADYHF 433

Qy     427 ICPALEFTKKFSEWGNNAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTK 486
           :|   |    :|  |   |:|::   ||: |||||:|  | ||:|||| |::|  |:
Db     434 LCQVNEMANAYSAAGQKVFYYHYTQVSSQSPWPEWVGAYHAAEIDFVFGQPMDRSKNFLP 493

Qy     487 AEEILSRSIVKRWANFAKYGNPN---ETQNNSTSWPVFKSTEQKYLTLNTE---STRIMT 540
             |  ||| ::: | |||| |:||   : |:    ||   :: ::|: |: :   : ::
Db     494 KEMELSRKMMRFWTNFAKTGDPNYDWDRQSAKNEWPSHTASGREYILLDAKHVHNFKVSK 553

Qy     541 KLRAQQCRFWTSFFPKVL----EMTGNI 564
           ||:::| ||  : |:::    |  |||
Db     554 GLRSKECAFWKEYLPQLVAATSEQYGNI 581


Search completed: January 30, 2003, 11:26:30
Job time : 41 secs
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09/748,
739

Inventor Search


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=> d his

     (FILE 'HOME' ENTERED AT 12:09:46 ON 30 JAN 2003)

     FILE 'HCAPLUS' ENTERED AT 12:09:53 ON 30 JAN 2003
                 E LOCKRIDGE/AU
L1            112 S E15-E18
                 E WATKINS J/AU
L2             80 S E39,E88,E96,E99-100
L3            191 S L1-2
L4          39023 S ?CHOLINESTERAS?
L5             97 S L3 AND L4
L6             72 S L5 AND BUTYRYLCHOLINESTERASE
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72 citations

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L6 ANSWER 1 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:841320 HCAPLUS
TITLE: Specificity of Ethephon as a **Butyrylcholinesterase** Inhibitor and Phosphorylating Agent
AUTHOR(S): Haux, J. Eric; **Lockridge, Oksana**; Casida, John E.
CORPORATE SOURCE: Environmental Chemistry and Toxicology Laboratory, Department of Environmental Science, Policy and Management, University of California, Berkeley, CA, 94720-3112, USA
SOURCE: Chemical Research in Toxicology (2002), 15(12), 1527-1533
CODEN: CRTOEC; ISSN: 0893-228X
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Butyrylcholinesterase** (BChE) is inhibited by the plant growth regulator (2-chloroethyl)phosphonic acid (ethephon) as obsd. 25 yr ago both in vitro and in vivo in rats and mice and more recently in subchronic studies at low doses with human subjects. The proposed mechanism is phosphorylation of the BChE active site at S198 by ethephon dianion. The present study tests this hypothesis directly using [33P]ethephon and recombinant BChE (rBChE) with single amino acid substitutions and further evaluates if BChE is the most sensitive esterase target in vitro and with mice in vivo. [33P]Ethephon labels purified rBChE but not enzymically inactive diethylphosphoryl-rBChE (derivatized at S198 by preincubation with chlorpyrifos oxon) or several other esterases and proteins. Amino acid substitutions that greatly reduce rBChE sensitivity to ethephon are G117H and G117K in the oxyanion hole (which may interfere with hydrogen bonding between glycine-N-H and ethephon dianion) and A328F, A328W, and A328Y (perhaps by impeding access to the active site gorge). Other substitutions that do not affect sensitivity are D70N, D70K, D70G, and E197Q which are not directly involved in the catalytic triad. The effect of pH and buffer compn. on inhibition supports the hypothesis that ethephon dianion is the actual phosphorylating agent without activation by divalent cations. Human plasma BChE in vitro and mouse plasma BChE in vitro and in vivo are more sensitive to ethephon than any other esterases detected by butyrylthiocholine or 1-naphthyl acetate hydrolysis in native-PAGE. All mouse liver esterases obsd. are less sensitive than plasma BChE to ethephon in vitro and in vivo. More than a dozen other esterases examd. are 10-100-fold less sensitive than BChE to ethephon. Thus, BChE inhibition continues to be the most sensitive marker of ethephon exposure.
REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:637842 HCAPLUS
DOCUMENT NUMBER: 137:181600
TITLE: **Butyrylcholinesterase** variants with increased catalytic efficiency against cocaine and their analytical and therapeutic uses
INVENTOR(S): **Lockridge, Oksana; Watkins, Jeffry D.**; Pancook, James D.
PATENT ASSIGNEE(S): Applied Molecular Evolution, Inc., USA; University of Nebraska Medical Center
SOURCE: PCT Int. Appl., 150 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002064796	A2	20020822	WO 2001-US50450	20011221
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2002119489	A1	20020829	US 2000-748739	20001226

PRIORITY APPLN. INFO.: US 2000-748739 A2 20001226
US 2001-32233 A2 20011220

AB The invention provides twenty-five **butyrylcholinesterase** variants having increased cocaine hydrolysis activity as well as the corresponding encoding nucleic acids. The invention also provides libraries of **butyrylcholinesterase** variants as well as libraries of the corresponding nucleic acids encoding **butyrylcholinesterase** variants. The invention further provides methods of hydrolyzing a cocaine-based **butyrylcholinesterase** substrate as well as methods of treating a cocaine-induced condition. Variants showing rates of cocaine hydrolysis that are 1.5-100-fold higher than that of the wild-type human enzyme are described. Guidelines for optimization of catalytic activity and the design of new variants are also disclosed.

L6 ANSWER 3 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:577800 HCAPLUS
TITLE: Re-engineering **butyrylcholinesterase** as a cocaine hydrolase
AUTHOR(S): Sun, Hong; Pang, Yuan-Ping; **Lockridge, Oksana**; Brimijoin, Stephen
CORPORATE SOURCE: Department of Molecular Pharmacology and Experimental Therapeutics, Molecular Neuroscience Program, Mayo Clinic and Foundation for Medical Education and Research, Mayo Graduate School, Rochester, MN, USA
SOURCE: Molecular Pharmacology (2002), 62(2), 220-224
CODEN: MOPMA3; ISSN: 0026-895X
PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To address the problem of acute cocaine overdose, we undertook mol. engineering of **butyrylcholinesterase** (BChE) as a cocaine hydrolase so that modest doses could be used to accelerate metabolic clearance of this drug. Mol. modeling of BChE complexed with cocaine suggested that the inefficient hydrolysis (kcat = 4 min-1) involves a rotation toward the catalytic triad, hindered by Tyr332. To eliminate rotational hindrance and retain substrate affinity, we introduced two amino acid substitutions (Ala328Trp/Tyr332Ala). The resulting mutant BChE reduced cocaine burden in tissues, accelerated plasma clearance by 20-fold, and prevented cocaine-induced hyperactivity in mice. The

enzyme's kinetic properties (kcat = 154 min-1, KM = 18 .mu.M) satisfy criteria suggested previously for treating cocaine overdose (kcat > 120 min-1, KM < 30 .mu.M). This success demonstrates that computationally guided mutagenesis can generate functionally novel enzymes with clin. potential.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:567367 HCAPLUS
TITLE: Wild-type and A328W mutant human **butyrylcholinesterase** tetramers expressed in Chinese hamster ovary cells have a 16-hour half-life in the circulation and protect mice from cocaine toxicity
AUTHOR(S): Duysen, Ellen G.; Bartels, Cynthia F.; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, USA
SOURCE: Journal of Pharmacology and Experimental Therapeutics (2002), 302(2), 751-758
CODEN: JPETAB; ISSN: 0022-3565
PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Human **butyrylcholinesterase** (BChE) hydrolyzes cocaine to inactive metabolites. A mutant of human BChE, A328W, hydrolyzed cocaine 15-fold faster compared with wild-type BChE. Although the catalytic properties of human BChE secreted by Chinese hamster ovary (CHO) cells are identical to those of native BChE, a major difference became evident when the recombinant BChE was injected into rats and mice. Recombinant BChE disappeared from the circulation within minutes, whereas native BChE stayed in the blood for a week. Nondenaturing gel electrophoresis showed that the recombinant BChE consisted mainly of monomers and dimers. In contrast, native BChE is a tetramer. The problem of the short residence time was solved by finding a method to assemble the recombinant BChE into tetramers. Coexpression in CHO cells of BChE and 45 residues from the N terminus of the COLQ protein yielded 70% tetrameric BChE. The resulting purified recombinant BChE tetramers had a half-life of 16 h in the circulation of rats and mice. The 16-h half-life was achieved without modifying the carbohydrate content of recombinant BChE. The protective effect of recombinant wild-type and A328W mutant BChE against cocaine toxicity was tested by measuring locomotor activity in mice. Pretreatment with wild-type BChE or A328W tetramers at a dose of 2.8 units/g i.p. reduced cocaine-induced locomotor activity by 50 and 80%. These results indicate that recombinant human BChE could be useful for treating cocaine toxicity in humans.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:567362 HCAPLUS
TITLE: Cocaine metabolism accelerated by a re-engineered human **butyrylcholinesterase**
AUTHOR(S): Sun, Hong; Shen, Maryann L.; Pang, Yuan-Ping; **Lockridge, Oksana**; Brimijoin, Stephen
CORPORATE SOURCE: Molecular Neuroscience Program, Department of Molecular Pharmacology and Experimental Therapeutics, Mayo Foundation for Medical Education and Research,

Rochester, MN, USA
SOURCE: Journal of Pharmacology and Experimental Therapeutics (2002), 302(2), 710-716
CODEN: JPETAB; ISSN: 0022-3565
PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Plasma **butyrylcholinesterase** (BChE) is important in the metab. of cocaine, but natural human BChE has limited therapeutic potential for detoxication because of low catalytic efficiency with cocaine. Here we report pharmacokinetics of cocaine in rats treated with A328W/Y332A BChE, an excellent cocaine hydrolase designed with the aid of mol. modeling. Compared with wild-type BChE, this enzyme hydrolyzes cocaine with 40-fold improved kcat (154 min-1 vs. 4.1 min-1) and only slightly increased KM (18 .mu.M vs. 4.5 .mu.M). In rats given this hydrolase (3 mg/kg i.v.) 10 min before cocaine challenge (6.8 mg/kg i.v.), cocaine half-life was reduced from 52 min to 18 min. Mirroring the redns. of plasma cocaine were large increases in benzoic acid, a product of BChE-mediated cocaine hydrolysis. All other pharmacokinetic parameters confirmed a large, dose-dependent acceleration of cocaine removal by the injected cocaine hydrolase. These results show that A328W/Y332A, an efficient cocaine hydrolase in vivo as well as in vitro, might promote cocaine detoxication in a clin. setting.
REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 6 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:510928 HCAPLUS
DOCUMENT NUMBER: 137:290755
TITLE: DNA sequence of **butyrylcholinesterase** from the rat: expression of the protein and characterization of the properties of rat **butyrylcholinesterase**
AUTHOR(S): Boeck, Andreea Ticu; Schopfer, Lawrence M.; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Biochemical Pharmacology (2002), 63(12), 2101-2110
CODEN: BCPCA6; ISSN: 0006-2952
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The rat is the model animal for toxicity studies. **Butyrylcholinesterase** (BChE), being sensitive to inhibition by some organophosphorus and carbamate pesticides, is a biomarker of toxic exposure. The goal of this work was to characterize the purified rat BChE enzyme. The cDNA sequence showed eight amino acid differences between the active site gorge of rat and human BChE, six clustered around the acyl binding pocket and two below the active site serine. A prominent difference in rat was the substitution of arginine for leucine at position 286 in the acyl pocket. Wild-type rat BChE, the mutant R286L, wild-type human BChE, and the mutant L286R were expressed in CHO cells and purified. Arg 286 was found responsible for the resistance of rat BChE to inhibition by Triton X-100. Replacement of Arg 286 with leucine caused the affinity for Triton X-100 to increase 20-fold, making it as sensitive as human BChE to inhibition by Triton X-100. Wild-type rat BChE had an 8- to 9-fold higher Km for the pos. charged substrates butyrylthiocholine, acetylthiocholine, propionylthiocholine, benzoylcholine, and cocaine compared with wild-type human BChE. Wild-type rat BChE catalyzed turnover 2- to 7-fold more rapidly than human BChE, showing the highest turnover

with propionylthiocholine (201,000 min-1). Human BChE does not reactivate spontaneously after inhibition by echothiophate, but rat BChE reactivates with a half-life of 4.3 h. Human serum contains 5 mg/L of BChE and 0.01 mg/L of AChE. Male rat serum contains 0.2 mg/L of BChE and .apprx.0.2 mg/L of AChE.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 7 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:274702 HCAPLUS
DOCUMENT NUMBER: 137:2377
TITLE: Naturally occurring mutation, Asp70His, in human **butyrylcholinesterase**
AUTHOR(S): Boeck, Andreea Ticu; Fry, Debra L.; Sastre, Antonio; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Annals of Clinical Biochemistry (2002), 39(2), 154-156
CODEN: ACBOBU; ISSN: 0004-5632
PUBLISHER: Royal Society of Medicine Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB People with genetic variants of **butyrylcholinesterase** can have hours of prolonged apnea after a normal dose of succinylcholine or mivacurium. Serum samples from 308 persons living in mid-USA were phenotyped to identify the atypical and fluoride variants. Three hundred eight samples were analyzed for the K variant by DNA amplification, digestion with Mae III and gel electrophoresis. Amplified DNA from 16 samples was sequenced to identify mutations D70G, T243M and D70H. D70H represents a novel mutation, described here for the first time. Values for kcat and Km were detd. for the D70H mutant BChE expressed in 293T cells. This mutation is located in the peripheral anionic site of **butyrylcholinesterase**, where it causes a 10-fold decrease in binding affinity for pos. charged substrates. People homozygous for the Asp70His mutation are expected to have prolonged apnea in response to succinylcholine or mivacurium, similar to people with the Asp70Gly mutation.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:249202 HCAPLUS
DOCUMENT NUMBER: 137:73632
TITLE: **Acetylcholinesterase** knockouts establish central cholinergic pathways and can use **butyrylcholinesterase** to hydrolyze acetylcholine
AUTHOR(S): Mesulam, M.-M.; Guillozet, A.; Shaw, P.; Levey, A.; Duysen, E. G.; **Lockridge, O.**
CORPORATE SOURCE: Northwestern University, Cognitive Neurology and Alzheimer's Disease Center and Department of Neurology and Psychiatry, Chicago, IL, 60611, USA
SOURCE: Neuroscience (Oxford, United Kingdom) (2002), 110(4), 627-639
CODEN: NRSCDN; ISSN: 0306-4522
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Acetylcholinesterase** is one of the most prominent constituents of central cholinergic pathways. It terminates the synaptic action of

acetylcholine through hydrolysis and yields the choline moiety that is necessary for transmitter recycling. Despite these pivotal relationships, mice nullizygous for **acetylcholinesterase** established all principal anatomical components of central cholinergic pathways. No compensatory increase in the distribution of **butyrylcholinesterase** was detected. However, both the wild-type and nullizygous mice showed that **butyrylcholinesterase** enzyme activity extended to all parts of the brain receiving cholinergic innervation and that it could hydrolyze the acetylcholine surrogate acetylthiocholine. As opposed to **acetylcholinesterase** which was mostly of neuronal origin, **butyrylcholinesterase** appeared to be mostly of glial origin. These expts. lead to the unexpected conclusion that **acetylcholinesterase** is not necessary for the establishment of cholinergic pathways. They also show that **butyrylcholinesterase** can potentially substitute for **acetylcholinesterase** and that this enzyme is likely to play a constitutive (rather than just back-up) role in the hydrolysis of acetylcholine in the normal brain. The inhibition of **butyrylcholinesterase** may therefore provide a desirable feature of cholinergic therapies, including those aimed at treating Alzheimer's disease.

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:246267 HCAPLUS
DOCUMENT NUMBER: 136:365079
TITLE: The active site of human paraoxonase (PON1)
AUTHOR(S): Josse, Denis; **Lockridge, Oksana**; Xie, Weihua; Bartels, Cynthia F.; Schopfer, Lawrence M.; Masson, Patrick
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Journal of Applied Toxicology (2001), 21(Suppl. 1), S7-S11
CODEN: JJATDK; ISSN: 0260-437X
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Ideally the authors would like to treat people exposed to nerve agents with an enzyme that rapidly destroys nerve agents. The enzymes considered for such a role include human **butyrylcholinesterase** (BChE), **acetylcholinesterase** (AChE), carboxylesterase and paraoxonase (PON1). Success has been achieved in endowing BChE with the ability to hydrolyze organophosphates. The G117H mutant of BCHE hydrolyzes sarin and VX, whereas the double mutant G117H/E197Q hydrolyzes soman. However, the rates of organophosphate hydrolysis are slow and a faster organophosphate hydrolase is being sought. Native PON1 hydrolyzes paraoxon with a catalytic efficiency, of 2.4 .times. 106 M-1 min-1, and our goal is to improve the organophosphate hydrolase activity of PON1. To achieve this we need to identify the amino acids in the active site of PON1. Using site-directed mutagenesis and expression in human 293T cells, the authors have identified the following eight amino acids as being essential to PON1 activity: W280, H114, H133, H154, H242, H284, E52 and D53. Fluorescence of PON1 complexed to terbium ion shows that at least one tryptophan is close to the calcium binding site.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:211553 HCAPLUS

DOCUMENT NUMBER: 136:397732
TITLE: Substrate activation in **acetylcholinesterase** induced by low pH or mutation in the .pi.-cation subsite
AUTHOR(S): Masson, Patrick; Schopfer, Lawrence M.; Bartels, Cynthia F.; Froment, Marie-Therese; Ribes, Fabien; Nachon, Florian; **Lockridge, Oksana**
CORPORATE SOURCE: Unite d'Enzymologie, Centre de Recherches du Service de Sante des Armees, La Tronche, Fr.
SOURCE: Biochimica et Biophysica Acta (2002), 1594(2), 313-324
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Substrate inhibition is considered a defining property of **acetylcholinesterase** (AChE), whereas substrate activation is characteristic of **butyrylcholinesterase** (BuChE). To understand the mechanism of substrate inhibition, the pH dependence of acetylthiocholine hydrolysis by AChE was studied between pH 5 and 8. Wild-type human AChE and its mutants Y337G and Y337W, as well as wild-type Bungarus fasciatus AChE and its mutants Y333G, Y333A and Y333W were studied. The pH profile results were unexpected. Instead of substrate inhibition, wild-type AChE and all mutants showed substrate activation at low pH. At high pH, there was substrate inhibition for wild-type AChE and for the mutant with tryptophan in the .pi.-cation subsite, but substrate activation for mutants contg. small residues, glycine or alanine. This is particularly apparent in the B. fasciatus AChE. Thus a single amino acid substitution in the .pi.-cation site, from the arom. tyrosine of B. fasciatus AChE to the alanine of BuChE, caused AChE to behave like BuChE. Excess substrate binds to the peripheral anionic site (PAS) of AChE. The finding that AChE is activated by excess substrate supports the idea that binding of a second substrate mol. to the PAS induces a conformational change that reorganizes the active site.
REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 11 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:108304 HCAPLUS
DOCUMENT NUMBER: 136:179804
TITLE: Engineering of a monomeric and low-glycosylated form of human **butyrylcholinesterase**. Expression, purification, characterization and crystallization
AUTHOR(S): Nachon, Florian; Nicolet, Yvain; Viguie, Nathalie; Masson, Patrick; Fontecilla-Camps, Juan C.; **Lockridge, Oksana**
CORPORATE SOURCE: Centre de Recherches du Service de Sante des Armees, Unite d'Enzymologie, La Tronche, 38702, Fr.
SOURCE: European Journal of Biochemistry (2002), 269(2), 630-637
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Blackwell Publishing Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Human **butyrylcholinesterase** (BChE; EC 3.1.1.8) is of particular interest because it hydrolyzes or scavenges a wide range of toxic compds. including cocaine, organophosphorus pesticides, and nerve agents. The relative contribution of each N-linked glycan for the soly., the stability, and the secretion of the enzyme was investigated. A recombinant monomeric BChE lacking 4 out of 9 N-glycosylation sites and the C-terminal oligomerization domain was stably expressed as a monomer in

CHO cells. The purified recombinant BChE showed catalytic properties similar to those of the native enzyme. Tetragonal crystals suitable for x-ray crystallog. studies were obtained; they were improved by recrystn. and found to diffract to 2.0 .ANG. resoln. using synchrotron radiation. The crystals were found to belong to tetragonal space group I422 with unit cell dimensions a = b = 154.7, c = 124.9 .ANG., giving a Vm of 2.73 .ANG.3 per Da (estd. 60% solvent) for a single mol. of recombinant BChE in the asym. unit. The crystal structure of BChE will help elucidate unsolved issues concerning ChE mechanisms in general.

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 12 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:789940 HCAPLUS
DOCUMENT NUMBER: 135:353984
TITLE: Evidence for **nonacetylcholinesterase** targets of organophosphorus nerve agent: supersensitivity of **acetylcholinesterase** knockout mouse to VX lethality
AUTHOR(S): Duysen, Ellen G.; Li, Bin; Xie, Weihua; Schopfer, Lawrence M.; Anderson, Robert S.; Broomfield, Clarence A.; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, USA
SOURCE: Journal of Pharmacology and Experimental Therapeutics (2001), 299(2), 528-535
CODEN: JPETAB; ISSN: 0022-3565
PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The possibility that organophosphate toxicity is due to inhibition of targets other than **acetylcholinesterase** (AChE, EC 3.1.1.7) was examd. in AChE knockout mice. Mice (34-55 days old) were grouped for this study, after it was detd. that AChE, **butyrylcholinesterase** (BChE), and carboxylesterase activities had reached stable values by this age. Mice with 0, 50, or 100% AChE activity were treated s.c. with the nerve agent VX. The LD50 for VX was 10 to 12 .mu.g/kg in AChE-/-, 17 .mu.g/kg in AChE+/-, and 24 .mu.g/kg in AChE+/+ mice. The same cholinergic signs of toxicity were present in AChE-/- mice as in wild-type mice, even though AChE-/- mice have no AChE whose inhibition could lead to cholinergic signs. Wild-type mice, but not AChE-/- mice, were protected by pretreatment with atropine. Tissues were extd. from VX-treated and untreated animals and tested for AChE, BChE, and acylpeptide hydrolase activity. VX treatment inhibited 50% of the AChE activity in brain and muscle of AChE+/+ and +/- mice, 50% of the BChE activity in all three AChE genotypes, but did not significantly inhibit acylpeptide hydrolase activity. It was concluded that the toxicity of VX must be attributed to inhibition of **nonacetylcholinesterase** targets in the AChE-/- mouse. Organophosphorus ester toxicity in wild-type mice is probably due to inhibition or binding to several proteins, only one of which is AChE.

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:244517 HCAPLUS
DOCUMENT NUMBER: 134:320816
TITLE: Predicted Michaelis-Menten complexes of cocaine-**butyrylcholinesterase**: engineering effective **butyrylcholinesterase** mutants for cocaine

detoxication
AUTHOR(S): Sun, Hong; El Yazal, Jamal; **Lockridge, Oksana** ; Schopfer, Lawrence M.; Brimijoin, Stephen; Pang, Yuan-Ping
CORPORATE SOURCE: Molecular Neuroscience Program, Mayo Foundation for Medical Education and Research, Rochester, MN, 55905, USA
SOURCE: Journal of Biological Chemistry (2001), 276(12), 9330-9336
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Butyrylcholinesterase** (BChE) is important in cocaine metab., but it hydrolyzes (-)-cocaine only one-two thousandth as fast as the unnatural (+)-stereoisomer. A starting point in engineering BChE mutants that rapidly clear cocaine from the bloodstream, for overdose treatment, is to elucidate structural factors underlying the stereochem. difference in catalysis. Here, the authors report two three-dimensional Michaelis-Menten complexes of BChE liganded with natural and unnatural cocaine mols., resp., that were derived from mol. modeling and supported by exptl. studies. Such complexes revealed that the benzoic ester group of both cocaine stereoisomers must rotate toward the catalytic Ser198 for hydrolysis. Rotation of (-)-cocaine appears to be hindered by interactions of its Ph ring with Phe329 and Trp430. These interactions do not occur with (+)-cocaine. Because the rate of (-)-cocaine hydrolysis is predicted to be detd. mainly by the re-orientation step, it should not be greatly influenced by pH. In fact, measured rates of this reaction were nearly const. over the pH range from 5.5 to 8.5, despite large rate changes in hydrolysis of (+)-cocaine. The authors' models can explain why BChE hydrolyzes (+)-cocaine faster than (-)-cocaine, and they suggest that mutations of certain residues in the catalytic site could greatly improve catalytic efficiency and the potential for detoxication.
REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 14 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:44255 HCAPLUS
DOCUMENT NUMBER: 134:291988
TITLE: Effects of mutations of active site residues and amino acids interacting with the .OMEGA. loop on substrate activation of **butyrylcholinesterase**
AUTHOR(S): Masson, P.; Xie, W.; Froment, M.-T.; **Lockridge, O.**
CORPORATE SOURCE: Centre de Recherches du Service de Sante des Armees, Unite d'Enzymologie, La Tronche, 38702, Fr.
SOURCE: Biochimica et Biophysica Acta (2001), 1544(1-2), 166-176
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The peripheral anionic site (PAS) of human **butyrylcholinesterase** is involved in the mechanism of substrate activation by pos. charged substrates and ligands. Two substrate binding loci, D70 in the PAS and W82 in the active site, are connected by the .OMEGA. loop. To det. whether the .OMEGA. loop plays a role in the signal transduction between the PAS and the active site, residues involved in stabilization of the loop, N83, K339 and W430, were mutated.. Mutations N83A and N83Q caused

loss of substrate activation, suggesting that N83 which interacts with the D70 backbone may be an element of the transducing system. The K339M and W430A mutant enzymes retained substrate activation. Residues W82, E197, and A328 in the active site gorge have been reported to be involved in substrate activation. At butyrylthiocholine concns. greater then 2 mM, W82A showed apparent substrate activation. Mutations E197Q and E197G strongly reduced substrate activation, while mutation E197D caused a moderate effect, suggesting that the carboxylate of residue E197 is involved in substrate activation. Mutations A328F and A328Y showed no substrate activation, whereas A328G retained substrate activation. Substrate activation can result from an allosteric effect due to binding of the second substrate mol. on the PAS. Mutation W430A was of special interest because this residue hydrogen bonds to W82 and Y332. W430A had strongly reduced affinity for tetramethylammonium. The bimol. rate const. for reaction with diisopropyl fluorophosphate was reduced 10,000-fold, indicating severe alteration in the binding area in W430A. The kcat values for butyrylthiocholine, o-nitrophenyl butyrate, and succinyldithiocholine were lower. This suggested that the mutation had caused misfolding of the active site gorge without altering the .OMEGA. loop conformation/dynamics. W430 as well as W231 and W82 appear to form the wall of the active site gorge. Mutation of any of these tryptophans disrupts the architecture of the active site.

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 15 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:618836 HCAPLUS
DOCUMENT NUMBER: 133:279464
TITLE: Abundant tissue **butyrylcholinesterase** and its possible function in the **acetylcholinesterase** knockout mouse
AUTHOR(S): Li, Bin; Stribley, Judith A.; Ticu, Andreea; Xie, Weihua; Schopfer, Lawrence M.; Hammond, Pamela; Brimijoin, Stephen; Hinrichs, Steven H.; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Journal of Neurochemistry (2000), 75(3), 1320-1331
CODEN: JONRA9; ISSN: 0022-3042
PUBLISHER: Lippincott Williams & Wilkins
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We have described recently an **acetylcholinesterase** (AChE) knockout mouse. While comparing the tissue distribution of AChE and **butyrylcholinesterase** (BChE), we found that extn. buffers contg. Triton X-100 strongly inhibited mouse BChE activity. In contrast, buffers with Tween 20 caused no inhibition of BChE. Conventional techniques grossly underestimated BChE activity by up to 15-fold. In Tween 20 buffer, the intestine, serum, lung, liver, and heart had higher BChE than AChE activity. Only brain had higher AChE than BChE activity in AChE +/+ mice. These findings contradict the dogma, based mainly on observations in Triton X-100 exts., that BChE is a minor **cholinesterase** in animal tissues. AChE +/- mice had 50% of normal AChE activity and AChE -/- mice had none, but all mice had similar levels of BChE activity. BChE was inhibited by Triton X-100 in all species tested, except rat and chicken. Inhibition was reversible and competitive with substrate binding. The active site of rat BChE was unique, having an arginine in place of leucine at position 286 (human BChE numbering) in the acyl-binding pocket of the active site, thus explaining the lack of inhibition of rat BChE by Triton X-100. The generally high levels of BChE

activity in tissues, including the motor endplate, and the observation that mice live without AChE, suggest that BChE has an essential function in nullizygous mice and probably in wild-type mice as well.

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 16 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:434881 HCAPLUS
DOCUMENT NUMBER: 133:234380
TITLE: Determination of the DNA sequences of **acetylcholinesterase** and **butyrylcholinesterase** from cat and demonstration of the existence of both in cat plasma
AUTHOR(S): Bartels, C. F.; Xie, W.; Miller-Lindholm, A. K.; Schopfer, L. M.; **Lockridge, O.**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Biochemical Pharmacology (2000), 60(4), 479-487
CODEN: BCPCA6; ISSN: 0006-2952
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Cat serum contains 0.5 mg/L of **butyrylcholinesterase** (BChE, EC 3.1.1.8) and 0.3 mg/L of **acetylcholinesterase** (AChE, EC 3.1.1.7); this can be compared with 5 mg/mL and < 0.01 mg/L, resp., in human serum. Cat BChE differed from human BChE in the steady-state turnover of butyrylthiocholine, having a 3-fold higher kcat and 2-fold higher Km and Kss values. Sequencing of the cat BCHE cDNA revealed 70 amino acid differences between cat and human BChE, three of which could account for these kinetic differences. These amino acids, which were located in the region of the active site, were Phe398Ile, Pro285Leu, and Ala277Leu (where the first amino acid was found in human and the second in cat). Sequencing genomic DNA for cat and human ACHE demonstrated that there were 33 amino acid differences between the cat and human AChE enzymes, but that there were no differences in the active site region. In addn., a polymorphism in intron 3 of the human ACHE gene was detected, as well as a silent polymorphism at Y116 of the cat ACHE gene.
REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 17 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:373729 HCAPLUS
DOCUMENT NUMBER: 133:130966
TITLE: Postnatal developmental delay and supersensitivity to organophosphate in gene-targeted mice lacking **acetylcholinesterase**
AUTHOR(S): Xie, Weihua; Stribley, Judith A.; Chatonnet, Arnaud; Wilder, Phillip J.; Rizzino, Angie; McComb, Rodney D.; Taylor, Palmer; Hinrichs, Steven H.; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, Department of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Omaha, NE, USA
SOURCE: Journal of Pharmacology and Experimental Therapeutics (2000), 293(3), 896-902
CODEN: JPETAB; ISSN: 0022-3565
PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Acetylcholinesterase** (AChE; EC 3.1.1.7) is the primary terminator of nerve impulse transmission at cholinergic synapses and is believed to play an important role in neural development. Targeted deletion of 4 exons of the ACHE gene reduced AChE activity by half in heterozygous mutant mice and totally eliminated AChE activity in nullizygous animals. **Butyrylcholinesterase** (EC 3.1.1.8) activity was normal in AChE -/- mice. Although nullizygous mice were born alive and lived up to 21 days, phys. development was delayed. The neuromuscular junction of 12-day-old nullizygous animals appeared normal in structure. Nullizygous mice were highly sensitive to the toxic effects of the organophosphate diisopropylfluorophosphate and to the **butyrylcholinesterase**-specific inhibitor bambuterol. These findings indicate that **butyrylcholinesterase** and possibly other enzymes are capable of compensating for some functions of AChE and that the inhibition of targets other than AChE by organophosphorus agents results in death.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 18 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:309111 HCAPLUS
DOCUMENT NUMBER: 133:85210
TITLE: Pesticides and susceptible populations: people with **butyrylcholinesterase** genetic variants may be at risk
AUTHOR(S): **Lockridge, Oksana**; Masson, Patrick
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Neurotoxicology (2000), 21(1 & 2), 113-126
CODEN: NRTXDN; ISSN: 0161-813X
PUBLISHER: Intox Press, Inc.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 107 refs. **Butyrylcholinesterase** (BChE) scavenges low doses of organophosphorus (for example, paraoxon) and carbamate pesticides (for example, carbaryl) and in this way protects people from the toxic effects of these poisons. The protective role of BChE is demonstrated by the finding that pesticide applicators can have reduced BChE activity with no clin. signs of poisoning. The question has arisen whether people with genetic variants of BChE are less protected. Seventy-six percent of the population is homozygous for wild-type BChE, while 24% carry at least one genetic variant allele. Most genetic variants of BChE have reduced activity. The clin. most important variant is atypical (D70G) BChE because people with this variant have 2 h of apnea after receiving a dose of succinylcholine that is intended to paralyze muscles for 3-5 min. In test tube expts. the atypical variant reacts more slowly with all pos. charged compds. (for example physostigmine, echothiophate). This leaves more toxin available for reaction with **acetylcholinesterase** in nerve synapses and predicts that people with atypical BChE will be less protected. Variants with low activity, such as silent BChE, are predicted to be at increased risk from organophosphorus pesticides based on expts. in monkeys and rodents where injection of purified BChE protected animals from the toxic effects of nerve agents. More studies are needed to strengthen the hypothesis that people with genetic variants of BChE are at higher risk of intoxication from pesticides.

REFERENCE COUNT: 107 THERE ARE 107 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 19 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:262893 HCAPLUS
DOCUMENT NUMBER: 133:101288
TITLE: Reaction of human **butyrylcholinesterase** (BChE) H117 enzymes with carbamates
AUTHOR(S): Broomfield, C. A.; Mills, K. V.; Meier, B. M.; **Lockridge, O.**; Millard, C. B.
CORPORATE SOURCE: U.S. Army Medical Research Institute of Chemical Defense, MD, 21010-5425, USA
SOURCE: Structure and Function of Cholinesterases and Related Proteins, [International Meeting on Cholinesterases and Related Proteins], 6th, La Jolla, CA, Mar. 20-24, 1998 (1998), 223-226. Editor(s): Doctor, Bhupendra P. Plenum Publishing Corp.: New York, N. Y.
CODEN: 68VDA8
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The authors discuss kinetic characterization of the G117H mutant of **butyrylcholinesterase** in an effort to better understand how this enzyme behaves with the intent of producing a better organophosphorus scavenger to protect military personnel against nerve agents.
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 20 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:262873 HCAPLUS
DOCUMENT NUMBER: 134:52127
TITLE: ACHE knockout mouse; cat AChE and cat BChE sequences; tetramers of BChE
AUTHOR(S): **Lockridge, Oksana**; Xie, Wei Hua; Chatonnet, Arnaud; Taylor, Palmer; Bartels, Cynthia F.; Altamirano, Cibby Varkey
CORPORATE SOURCE: Eppley Institute, University of Nebraska Med. Ctr., Omaha, NE, 68198-6805, USA
SOURCE: Structure and Function of Cholinesterases and Related Proteins, [International Meeting on Cholinesterases and Related Proteins], 6th, La Jolla, CA, Mar. 20-24, 1998 (1998), 41-44. Editor(s): Doctor, Bhupendra P. Plenum Publishing Corp.: New York, N. Y.
CODEN: 68VDA8
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Chimeric mice carrying the knocked out ACHE (**acetylcholinesterase**) gene were created. It was shown that the knockout was transmitted in the germline of at least one of chimeric mouse and that the heterozygote knockout is capable of living at least to 21 day of gestation, until the day of birth. Addnl. breeding may yield a live heterozygous mouse. However, the homozygous knockout is expected to be embryonic lethal. The DNA and deduced amino acid sequences of **butyrylcholinesterase** (BChE) and **acetylcholinesterase** (AChE) from domestic cat and the BChE from Bengal tiger was detd. Using the yeast two-hybrid system it was shown that the C-terminus of BChE is the tetramerization domain. Poly-L-proline added to culture medium of CHO cells expressing wild-type BChE increased the percentage of tetramers.
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 21 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:71826 HCAPLUS
DOCUMENT NUMBER: 132:204691

TITLE: The **butyrylcholinesterase** K-variant shows similar cellular protein turnover and quaternary interaction to the wild-type enzyme
AUTHOR(S): Altamirano, Cibby Varkey; Bartels, Cynthia F.; **Lockridge, Oksana**
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology and Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Journal of Neurochemistry (2000), 74(2), 869-877
CODEN: JONRA9; ISSN: 0022-3042
PUBLISHER: Lippincott Williams & Wilkins
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A recent study has linked the **butyrylcholinesterase** (BChE) K-variant and the apolipoprotein .epsilon.4 isoform to late-onset Alzheimer's disease. These findings have been controversial and have led us to examine the differences between wild-type and K-variant BChE in enzyme activity, protein stability, and quaternary structure. J-variant BChE (E497V/A539T) was also studied because it is assocd. with the K-variant mutation. The K-variant mutation (A539T) is located in the C-terminal tetramerization domain. Wild-type, K-variant, and J-variant BChE were expressed in Chinese hamster ovary cells and purified. The purified enzymes had similar binding affinity (Km) values and catalytic rates for butyrylthiocholine and benzoylcholine. In pulse-chase studies the K-variant, J-variant, and wild-type BChE were degraded rapidly within the cell, with a half-time of .apprx. 1.5h. Less than 5% of the intracellular BChE was exported. The C-terminal peptide contg. the K-variant mutation interacted with itself as strongly as did the wild-type peptide in the yeast two-hybrid system. Both K-variant and wild-type BChE assembled into tetramers in the presence of poly-L-proline or the proline-rich attachment domain of the collagen tail. The native K-variant BChE in serum showed the same proportion of tetramers as the native serum wild-type BChE. We conclude that the K-variant BChE is similar to wild-type BChE in enzyme activity, protein turnover, and tetramer formation.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 22 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:794264 HCAPLUS
DOCUMENT NUMBER: 132:32680
TITLE: Esterase mutants for detoxification of organophosphates
INVENTOR(S): Broomfield, Clarence A.; Millard, Charles B.; **Lockridge, Oksana**
PATENT ASSIGNEE(S): United States Dept. of the Army, USA
SOURCE: U.S., 64 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6001625	A	19991214	US 1995-446100	19950519

PRIORITY APPLN. INFO.: US 1995-446100 19950519

AB A method of modifying esterases by substitution with histidine of at least one amino acid within 6 .ANG. of an active site serine provides esterases useful for detoxifying organophosphates. Thus, G117H human

butyrylcholinesterase was produced. This mutant enzyme catalyzed the hydrolysis of VX at 25.degree. and pH 7.5 with turnover no. of 5 X 10-4 sec-1, a 350-fold increase over spontaneous hydrolysis under the same conditions. This enzyme was also able to hydrolyze sarin, DFP, methylphosphonothioate, and Echothiophate.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 23 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:606354 HCAPLUS
DOCUMENT NUMBER: 131:319606
TITLE: Interaction between the peripheral site residues of human **butyrylcholinesterase**, D70 and Y332, in binding and hydrolysis of substrates
AUTHOR(S): Masson, Patrick; Xie, Weihua; Froment, Marie-Therese; Levitsky, Vladislav; Fortier, Pierre-Louis; Albaret, Christine; **Lockridge, Oksana**
CORPORATE SOURCE: Centre de Recherches du Service de Sante des Armees, Unite d'Enzymologie, La Tronche, 38702, Fr.
SOURCE: Biochimica et Biophysica Acta (1999), 1433(1-2), 281-293
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Human **butyrylcholinesterase** displays substrate activation with pos. charged butyrylthiocholine (BTC) as the substrate. Peripheral anionic site (PAS) residues D70 and Y332 appear to be involved in the initial binding of charged substrates and in activation control. To det. the contribution of PAS residues to binding and hydrolysis of quaternary substrates and activation control, the single mutants D70G/Y and Y332F/A/D and the double mutants Y332A/D70G and Y332D/D70Y were studied. Steady-state hydrolysis of the charged substrates, BTC and succinyldithiocholine, and the neutral ester o-nitrophenyl butyrate was measured. In addn., inhibition of wild-type and mutant enzymes by tetramethylammonium was investigated, at low concns. of BTC. Single and double mutants of D70 and Y332 showed little or no substrate activation, suggesting that both residues were important for activation control. The effects of double mutations on D70 and Y332 were complex. Double-mutant cycle anal. provided evidence for interaction between these residues. The category of interaction (either synergistic, additive, partially additive or antagonistic) was found to depend on the nature of the substrate and on measured binding or kinetic parameters. This complexity reflects both the crosstalk between residues involved in the sequential formation of productive Michaelian complexes and the effect of peripheral site residues on catalysis. It is concluded that double mutations on the PAS induce a conformational change in the active site gorge of **butyrylcholinesterase** that can alter both substrate binding and enzyme acylation.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 24 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:577517 HCAPLUS
DOCUMENT NUMBER: 131:319580
TITLE: Conserved Aromatic Residues of the C-Terminus of Human **Butyrylcholinesterase** Mediate the Association of Tetramers
AUTHOR(S): Altamirano, Cibby Varkey; **Lockridge, Oksana**
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology and

Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Biochemistry (1999), 38(40), 13414-13422
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Human **butyrylcholinesterase** (BChE) in serum is composed predominantly of tetramers. The tetramerization domain of each subunit is contained within 40 C-terminal residues. To identify key residues within this domain participating in tetramer stabilization, the interaction between C-terminal 46 residue peptides was quantitated in the yeast two-hybrid system. The wild-type peptide interacted strongly with another wild-type peptide in the yeast two-hybrid system. The C571A mutant peptides interacted to a similar degree as the wild-type. However, the mutant in which seven conserved arom. residues (Trp 543, Phe 547, Trp 550, Tyr 553, Trp 557, Phe 561, and Tyr 564) and C571 were altered to alanines showed only 12% of the interaction seen with the wild-type peptide. The seven mutations (aroms.-off) were incorporated into the complete BChE mol., with or without the C571A mutation, and expressed in 293T and CHO-K1 cells. Expression of wild-type BChE in these cell lines yielded 10% tetramers. The aroms.-off mutant formed dimers and monomers but no tetramers. The aroms.-off/C571A mutant yielded only monomers. Addn. of poly-L-proline to culture medium, or coexpression with the N-terminus of COLQ including the proline-rich attachment domain (QNPRAD), increased the amt. of tetrameric wild-type BChE from 10 to 70%, but had no effect on the G534stop (lacking 41 C-terminal residues) and the aroms.-off mutants. Recombinant BChE produced by coexpression with QNPRAD was purified by column chromatog. The purified tetramers contained the FLAG-tagged QNPRAD peptide. These observations suggest that the stabilization of BChE tetramers is mediated through the interaction of the seven conserved arom. residues and that poly-L-proline and PRAD act through these arom. residues to induce tetramerization.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 25 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:486194 HCAPLUS
DOCUMENT NUMBER: 131:210933
TITLE: Protein engineering of a human enzyme that hydrolyzes V and G nerve agents: design, construction and characterization
AUTHOR(S): Broomfield, Clarence A.; **Lockridge, Oksana**; Millard, Charles B.
CORPORATE SOURCE: US Army Medical Research Institute of Chemical Defense, APG, MD, 21010-5425, USA
SOURCE: Chemico-Biological Interactions (1999), 119-120, 413-418
CODEN: CBINA8; ISSN: 0009-2797
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Because of deficiencies in the present treatments for organophosphorus **anticholinesterase** poisoning, we are attempting to develop a catalytic scavenger that can be administered as prophylactic protection. Currently known enzymes are inadequate for this purpose because they have weak binding and slow turnover, so we are trying to make an appropriate enzyme by protein engineering techniques. One **butyrylcholinesterase** mutant, G117H, has the desired type of activity but reacts much too slowly. This communication describes an

attempt to det. the reason for the slow reaction so that a more efficient enzyme might be designed. The results indicate that the mutation at residue 117 has resulted in a distortion of the transition state of the reaction of organophosphorus compds. with the active site serine. This information will be used to develop other mutants that avoid transition state stabilization sites.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 26 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:486155 HCAPLUS
DOCUMENT NUMBER: 131:210932
TITLE: Differences in active-site gorge dimensions of **cholinesterases** revealed by binding of inhibitors to human **butyrylcholinesterase**
AUTHOR(S): Saxena, Ashima; Redman, Ann M. G.; Jiang, Xuliang; **Lockridge, Oksana**; Doctor, B. P.
CORPORATE SOURCE: Division of Biochemistry, Walter Reed Army Institute of Research, Washington, DC, 20307, USA
SOURCE: Chemico-Biological Interactions (1999), 119-120, 61-69
CODEN: CBINA8; ISSN: 0009-2797
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We examd. the role of A328(F330) in the binding of various inhibitors to **cholinesterases** (ChEs) using human **butyrylcholinesterase** (BChE) mutants to det. if the conclusions drawn from studies with **acetylcholinesterase** (AChE) mutants could be extended to BChE. For huperzine A and edrophonium, the results obtained with AChE mutants could be directly correlated with those obtained with native ChEs and site-specific mutants of human BChE. Inhibition studies of ethopropazine with BChE mutants, where A328 was modified to either F or Y, suggested that A328 was not solely responsible for the selectivity of ethopropazine. Vol. calcns. for the active-site gorge showed that the poor inhibitory activity of ethopropazine towards AChE was due to the smaller dimension of the active-site gorge. The vol. of the BChE active-site gorge is .apprxeq. 200 .ANG.3 larger than that of the AChE gorge, which allows the accommodation of ethopropazine in two different orientations as demonstrated by rigid-body refinement and mol. dynamics calcns. These results suggest that, although the overall scaffolding of the two enzymes may be highly similar, the dimensions and the micro-environment of the gorge play a significant role in detg. the selectivity of substrate and inhibitors for ChEs.
REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 27 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:486154 HCAPLUS
DOCUMENT NUMBER: 131:210931
TITLE: Association of tetramers of human **butyrylcholinesterase** is mediated by conserved aromatic residues of the carboxy terminus
AUTHOR(S): Altamirano, Cibby Varkey; **Lockridge, Oksana**
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Chemico-Biological Interactions (1999), 119-120, 53-60
CODEN: CBINA8; ISSN: 0009-2797
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal

LANGUAGE: English

AB Human **butyrylcholinesterase** (BChE) is composed predominantly of tetramers. Up to 40 C-terminal residues of each subunit contribute to the stabilization of tetramers. To better define the residues which participate in tetramer stabilization, the in vivo interaction of the BChE C-terminus 46-residue peptide was quantitated for wild type and mutant BChE using the yeast two-hybrid system. The wild type C-terminal peptides interacted with one another in this system. The K-variant (A539T) and C571A peptides showed interaction similar to that of the wild type. However, only 11.7% of the interaction seen with the wild type peptide was obsd. with the mutant in which 7 conserved arom. residues (Trp 543, Phe 547, Trp 550, Tyr 553, Trp 557, Phe 561, and Tyr 564) had been altered to alanines (aroms. off mutant).. When these 7 mutations were incorporated into the complete BChE mol. and expressed in 293T cells, only monomers and dimers were obsd. The addn. of poly-L-proline to the medium of 293T cells expressing wild type BChE resulted in the increase of the tetrameric form, similar to that obsd. by S. Bon et al. (1997) for **acetylcholinesterase** expressed in COS cells. However, no increase in tetramers was obsd. with poly-L-proline addn. to the medium of 293T cells expressing the aroms. off BChE mutant. These observations suggest that the stabilization of BChE tetramers is mediated through the interaction of the 7 conserved arom. residues, Trp 543, Phe 547, Trp 550, Tyr 553, Trp 557, Phe 561, and Tyr 564, and that the poly-L-proline induced increase in tetrameric BChE is mediated through these 7 arom. residues.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 28 OF 72 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1999:486151 HCAPLUS

DOCUMENT NUMBER: 131:210930

TITLE: Structural and hydration changes in the active site gorge of phosphorylated **butyrylcholinesterase** accompanying the aging process

AUTHOR(S): Masson, Patrick; Fortier, Pierre-Louis; Albaret, Christine; Clery, Cecile; Guerra, Patrice; **Lockridge, Oksana**

CORPORATE SOURCE: Centre de Recherches du Service de Sante des Armees, Unite d'Enzymologie, La Tronche, 38702, Fr.

SOURCE: Chemico-Biological Interactions (1999), 119-120, 17-27
CODEN: CBINA8; ISSN: 0009-2797

PUBLISHER: Elsevier Science Ireland Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Wild-type (wt) **butyrylcholinesterase** (BuChE) and the E197D and D70G mutants were inhibited by diisopropylfluorophosphate (DFP) or soman under std. conditions of pH, temp. and pressure. The effect of hydrostatic and osmotic pressures on the aging process of DFP-phosphorylated enzymes (diisopropylphosphoryl-BuChE (DIP-BuChE)) was investigated. Hydrostatic pressure strongly increased the rate of aging of wt enzyme. The activation vols. (.DELTA.V) for the dealkylation reaction was -150 mL/mol for DIP-wt-BuChE. On the other hand, pressure had little effect on the aging of the DIP-E197D mutant and no effect on the DIP-D70G mutant, indicating that the transition state of the aging reaction (dealkylation of an isoproxy chain) was assocd. with an extended conformation/ hydration change in wtBuChE but not in mutants. The rate of aging decreased with osmotic pressure, supporting the idea that water is important for stabilizing the transition state. Mol. dynamics simulations were performed on the wtDIP adduct to relate the kinetic data to hydration changes in the enzyme active site gorge. The pH dependence of the melting

temp. (Tm) of native and soman-wtBuChE, as detd. by differential scanning calorimetry (DSC), indicated that the stabilization energy of aged BuChE is mainly due to the salt bridge between protonated H438 and PO-, with pKH438 = 8.3. Electrophoresis under high pressure up to 2.5 kbar showed that aged wtBuChE did not undergo pressure-induced molten globule transition unlike the native enzyme. This transition was not seen for the mutant enzymes, indicating that mutants are resistant to the penetration of water into their structure. Our results support the conclusion that D70 and E197 are major residues for the water/H-bond network dynamics in the active site gorge of BuChE, both residues acting like valves. In mutant enzymes, mutated residues function like check valves: forced penetration of water in the gorge is difficult, release of water is facilitated.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 29 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:340915 HCAPLUS
DOCUMENT NUMBER: 131:126586
TITLE: Mechanical aspects of the phosphotriesterase activity of **butyrylcholinesterase** G117H mutant
AUTHOR(S): Albaret, Christine; Masson, Patrick; Broomfield, Clarence A.; **Lockridge, Oksana**; Fortier, Pierre-Louis
CORPORATE SOURCE: Laboratoire de RMN et Modelisation Moleculaire, Centre d'Etudes du Bouchet, Vert-le-Petit, 91710, Fr.
SOURCE: Proceedings of the ERDEC Scientific Conference on Chemical and Biological Defense Research, Aberdeen Proving Ground, Md., Nov. 18-21, 1997 (1998), Meeting Date 1997, 889-894. Editor(s): Berg, Dorothy A. National Technical Information Service: Springfield, Va.
CODEN: 67QJAS
DOCUMENT TYPE: Conference
LANGUAGE: English

AB The G117H mutant of human **butyrylcholinesterase** is able to catalyze the hydrolysis of organophosphate esters paraoxon and echothiophate. In order to understand this property, a mol. mechanic study of the mutant adduct was carried out. When the imidazole ring was protonated on the N.delta.1 site, the bonded hydrogen was found to bridge the two alkoxy oxygens of the phosphorylated serine in the min. energy conformation. This conformation was shown to be very stable during mol. dynamics. In particular, the phosphoryl oxygen was found to make strong hydrogen bonds with the oxyanion hole, resulting in the weakening of the O.gamma.-P bond to be broken. The pos. electrostatic field generated by H117 and the adjacent protonated H438 could attract and direct a water mol. for nucleophilic attack and subsequent dephosphorylation. The double hydrogen-bonding of alkoxy oxygens may account for the faster aging of G117H mutant when compared to the wild-type enzyme. When the imidazole ring was protonated on the N.epsilon.2 site, the position of H117 ring in the min. energy conformation was similar to that found for the other protonation site. In this case, the specific position of the H117 ring could allow a direct attack of nitrogen N.delta.1 on the phosphorus atom, the resulting phosphoenzyme intermediate being cleaved by a water mol. in a second reaction to regenerate the active enzyme.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 30 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:85111 HCAPLUS

DOCUMENT NUMBER: 130:219766
TITLE: Polyol-induced activation by excess substrate of the D70G **butyrylcholinesterase** mutant
AUTHOR(S): Levitsky, Vladislav; Xie, Weihua; Froment, Marie-Therese; **Lockridge, Oksana**; Masson, Patrick
CORPORATE SOURCE: Unite d'Enzymologie, Centre de Recherches du Service de Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Biochimica et Biophysica Acta (1999), 1429(2), 422-430
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Wild-type human **butyrylcholinesterase** (BuChE) has a non-Michaelian behavior showing substrate activation with butyrylthiocholine (BTC) as the substrate. The D70G mutant has a catalytic const. identical to that of the wild-type enzyme, but a 10-fold lower affinity for BTC compared to wild-type enzyme, and it does not exhibit activation by excess BTC under conventional conditions. In the present work it was found that addn. of polyols or sugars changed the kinetic behavior of the D70G mutant with BTC. In the presence of 40% sucrose, the D70G mutant enzyme displayed marked activation by excess substrate. Because D70 is hydrogen bonded to Y332, mutants of Y332 were studied. Mutant Y332F had a behavior similar to that of wild-type BuChE, whereas mutants Y332A, Y332A/D70G and D70G had negligible substrate activation. The behavior of wild-type, Y332F, Y332A and Y332A/D70G did not change in the presence of high concns. of sugar. Substrate activation has been explained by binding of a second substrate mol. in the peripheral site at D70. The D70G mutant should be incapable of substrate activation, if D70 were the only residue involved in substrate activation. The ability of the D70G mutant to display substrate activation by medium engineering suggests that other residues are involved in initial substrate binding and activation by excess substrate. Osmolyte-induced change in conformation and/or hydration status of Y332 and other solvent-exposed residues may account for the non-Michaelian behavior of the D70G mutant.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 31 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:36651 HCAPLUS
DOCUMENT NUMBER: 130:193573
TITLE: An improved cocaine hydrolase: the A328Y mutant of human **butyrylcholinesterase** is 4-fold more efficient
AUTHOR(S): Xie, Weihua; Altamirano, Cibby Varkey; Bartels, Cynthia F.; Speirs, Robert J.; Cashman, John R.; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute and Department of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Omaha, NE, USA
SOURCE: Molecular Pharmacology (1999), 55(1), 83-91
CODEN: MOPMA3; ISSN: 0026-895X
PUBLISHER: American Society for Pharmacology and Experimental Therapeutics
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Butyrylcholinesterase** (BChE) plays a major role in cocaine detoxification. The rate at which human BChE hydrolyzes cocaine is slow, with a kcat of 3.9 min-1 and Km of 14 .mu.M. The authors' goal was to improve the cocaine hydrolase activity of BChE by mutating residues near

the active site. Mutant A328Y had a kcat of 10.2 min-1 and Km of 9 .mu.M for a 4-fold improvement in catalytic efficiency (kcat/Km). Since benzoylcholine (kcat, 15,000 min-1) and cocaine form the same acyl-enzyme intermediate but are hydrolyzed at 4000-fold different rates, it was concluded that a step leading to formation of the acyl-enzyme intermediate was rate-limiting. BChE purified from plasma of cat, horse, and chicken was tested for cocaine hydrolase activity. Compared with human BChE, horse BChE had a 2-fold higher kcat but a lower binding affinity; cat BChE was similar to human BChE; and chicken BChE had only 10% of the catalytic efficiency. Naturally occurring genetic variants of human BChE were also tested for cocaine hydrolase activity. The J and K variants (E497V and A539T) had kcat and Km values similar to wild-type BChE, but because these variants are reduced to 66 and 33% of normal levels in human blood, resp., people with these variants may be at risk for cocaine toxicity. The atypical variant (D70G) had a 10-fold lower binding affinity for cocaine, suggesting that persons with the atypical variant of BChE may experience severe or fatal cocaine intoxication when administered a dose of cocaine that is not harmful to others.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 32 OF 72 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:636304 HCAPLUS

DOCUMENT NUMBER: 130:11392

TITLE: The pH Dependence of Dealkylation in Soman-Inhibited **Cholinesterases** and Their Mutants: Further Evidence for a Push-Pull Mechanism

AUTHOR(S): Saxena, Ashima; Viragh, Carol; Frazier, D. Scott; Kovach, Ildiko M.; Maxwell, Donald M.; **Lockridge, Oksana**; Doctor, B. P.

CORPORATE SOURCE: Division of Biochemistry, Walter Reed Army Institute of Research, Washington, DC, 20307, USA

SOURCE: Biochemistry (1998), 37(43), 15086-15096
CODEN: BICHAW; ISSN: 0006-2960

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Bimol. rate consts. for the inactivation of recombinant (r) human (Hu) **butyrylcholinesterase** (BChE) with P(S)C(S)- and P(S)C(R)-2-(3,3-dimethylbutyl) methylphosphonofluoridate (soman) are (92.+-.7) .times. 106 M-1 min-1 and (13.7.+-.0.8) .times. 106 M-1 min-1 at pH 7.4, .mu. = 0.1 M and 25.degree.. Mutations of E197(199) to D or Q and W82(84) to A result in redns. in the rate consts. for inactivation with P(S)C(S)-soman 4.3-, 11.8-, and 263-fold and with P(S)C(R)-soman by 6.5-, 47.3-, and 685-fold, resp. The pH dependence of dealkylation (aging) in r mouse (Mo) **acetylcholinesterase** (AChE) and rHu BChE and their mutants inactivated with P(S)C(S)- and P(S)C(R)-soman was compared. Best-fit parameters for the asym. bell curves for the adducts of wild-type Mo AChE are pK1 = pK2 = 4.0-4.9 and pK3 = 5.2-6.6. These pKs are consistent with the involvement of two carboxylic acids, possibly E202(199) and either E334(327) or E450(443), and H447(440)H+ in the dealkylation of AChE. E202Q MoAChE inactivated with the soman diastereomers yielded pK3 = 5.5-5.8. Nearly sym. pH curves for soman-inhibited wild-type and E197D Hu BChE gave pK2 = 3.7-4.6 and pK3 = 7.3-8.0, but much lower, pK3 .apprx. 5, for the corresponding adduct of the E197Q mutant. Dealkylation in soman-inhibited BChE is consistent with the participation of one carboxylic acid side chain and H438(440)H+. Maximal rate consts. for dealkylation (kmax) are 1-6 min-1 for AChE and 2 min-1 for BChE at 25.degree.. The W82 to A mutation in BChE results in the largest redn., 2500-6000-fold, in the rate const. for dealkylation.

The redn. in the rate consts. for dealkylation in the E197 mutants is highly pH dependent. The solvent isotope effects at the pH maxima are 1.3-1.4, indicating unlikely preprotonation or proton in "flight" at the enzymic transition states. The new results support the push-pull mechanism of dealkylation in soman-inhibited **cholinesterases** proposed previously.

REFERENCE COUNT: 77 THERE ARE 77 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 33 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:579318 HCAPLUS
DOCUMENT NUMBER: 130:1625
TITLE: Resistance of **butyrylcholinesterase** to inactivation by ultrasound: effects of ultrasound on catalytic activity and subunit association
AUTHOR(S): Froment, Marie-Therese; **Lockridge, Oksana**; Masson, Patrick
CORPORATE SOURCE: Unite d'Enzymologie, Centre de Recherches du Service de Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Biochimica et Biophysica Acta (1998), 1387(1-2), 53-64
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The effects of 20 kHz ultrasound on catalytic activity and structure of the tetramer of wild-type human **butyrylcholinesterase** (BChE) from plasma and recombinant D70G mutant enzyme were studied at const. temp. Effects on catalytic properties of both enzymes were investigated by kinetic anal. under ultrasound irradn. using a neutral substrate (o-nitrophenylbutyrate), a pos. charged substrate (butyrylthiocholine), and a neg. charged substrate (aspirin). Effects on structure of highly purified wild-type BChE were followed by gel electrophoresis and activity measurements at Vmax after ultrasound treatment. Unlike hydrostatic pressure, mild ultrasound had moderate effects on catalytic parameters of BChE-catalyzed hydrolysis of substrates. For both wild-type and D70G, Km increased slightly with butyrylthiocholine and o-nitrophenylbutyrate under ultrasound irradn., suggesting that these effects of ultrasound were not due to the periodic variation of pressure but rather to shear forces that took off substrate from the peripheral site and altered diffusion to the active site. By contrast, affinity of the D70G mutant for aspirin slightly increased with ultrasound power, suggesting that ultrasound-induced microstreaming unmasked peripheral residues involved in recognition and initial binding of the neg. charged substrate. Results support the contention that Km is a composite affinity const., including dissocn. const. of the first encounter enzyme-substrate complex on the peripheral site. Small changes in catalytic activity may have resulted from ultrasound-induced subtle conformational changes altering the active site reactivity. Short ultrasound irradn. induced a faint transient enzyme activation, but prolonged irradn. caused partial dissocn. of the tetrameric enzyme and irreversible inactivation. Partial dissocn. was related to enzyme microheterogeneity, i.e., nicked (C-terminal segment depleted) tetramers were less stable than native tetramers. The resistance of the native tetramer to ultrasound-induced dissocn. was ascribed to the existence of an arom. amino acid array on the apolar side of the C-terminal helical segment of subunits, the four subunits being held together in a four-helix bundle contg. the arom. zipper motifs. Arom./arom. interactions between the four helical segments are thought to be enhanced by ultrasound-generated pressure.

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 34 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:579317 HCAPLUS
DOCUMENT NUMBER: 130:10271
TITLE: **Butyrylcholinesterase**-catalyzed hydrolysis of aspirin, a negatively charged ester, and aspirin-related neutral esters
AUTHOR(S): Masson, Patrick; Froment, Marie-Therese; Fortier, Pierre-Louis; Visicchio, Jean-Emmanuel; Bartels, Cynthia F.; **Lockridge, Oksana**
CORPORATE SOURCE: Unite d'Enzymologie, Centre de Recherches du Service de Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Biochimica et Biophysica Acta (1998), 1387(1-2), 41-52
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Although aspirin (acetylsalicylic acid) is neg. charged, it is hydrolyzed by **butyrylcholinesterase** (BuChE). Catalytic parameters were detd. in 100 mM Tris buffer, pH 7.4, in the presence and absence of metal cations. The presence of Ca2+ or Mg2+ (<100 mM) in buffer did not change the Km, but accelerated the rate of hydrolysis of aspirin by wild-type or D70G mutant BuChE by 5-fold. Turnover nos. were of the order of 5000-12000 min-1 for the wild-type enzyme and the D70G and D70K enzymes in 100 mM Tris, pH 7.4, contg. 50 mM CaCl2 at 25.degree.C; Km values were 6 mM for wild-type, 16 mM for D70G and 38 mM for D70K. People with 'atypical' BuChE have the D70G mutation. The apparent inhibition seen at high aspirin concn. was not due to inhibition by excess substrate but to spontaneous hydrolysis of aspirin, causing inhibition by salicylate. The wild-type and D70G enzymes were competitively inhibited by salicylic acid; the D70K enzyme showed a complex parabolic inhibition, suggesting multiple binding. The effect of salicylate was substrate-dependent, the D70K mutant being activated by salicylate with butyrylthiocholine as substrate. Km value for wild-type enzyme was lower than for D70 mutants, suggesting that residue 70 located at the rim of the active site gorge was not the major site for the initial encounter aspirin-BuChE complex. On the other hand, the virtual absence of affinity of the W82A mutant for aspirin indicated that W82 was the major residue involved in formation of the Michaelis complex. Mol. modeling of aspirin binding to BuChE indicated perpendicular interactions between the arom. rings of W82 and aspirin. Kinetic study of BuChE-catalyzed hydrolysis of different acetyl esters showed that the rate limiting step was acetylation. The bimol. rate consts. for hydrolysis of aspirin by wild-type, D70G and D70K enzymes were found to be close to 1.times.106 M-1 min-1. These results support the contention that the electrostatic steering due to the neg. electrostatic field of the enzyme plays a role in substrate binding, but plays no role in the catalytic steps, i.e. in the enzyme acetylation.
REFERENCE COUNT: 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 35 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:412993 HCAPLUS
DOCUMENT NUMBER: 129:145761
TITLE: Reaction of human **butyrylcholinesterase** (BCHE) H117 enzymes with carbamates
AUTHOR(S): Broomfield, C. A.; Mills, K. V.; Meier, B. M.; **Lockridge, O.**; Millard, C. M.
CORPORATE SOURCE: U.S. Army Medical Research Institute of Chemical Defense APG, MD, 21010-5425, USA
SOURCE: Nucleic Acids Symposium Series (1998), 38(Advances in

Gene Technology: Molecular Biology in the Conquest of Disease), 165-166
CODEN: NACSD8; ISSN: 0261-3166
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The reactions of physostigmine and pyridostigmine with human **butyrylcholinesterase** were described.
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 36 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:139392 HCAPLUS
TITLE: Mechanical aspects of the phosphotriesterase activity of **butyrylcholinesterase** G117H mutant.
AUTHOR(S): Fortier, P. L.; Albaret, C.; Masson, P.; Broomfield, C. A.; **Lockridge, O.**
CORPORATE SOURCE: Centre d'Etudes du Bouchet - DGA, Vert-le-Petit, 91710, Fr.
SOURCE: Book of Abstracts, 215th ACS National Meeting, Dallas, March 29-April 2 (1998), COMP-196. American Chemical Society: Washington, D. C.
CODEN: 65QTAA
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB The G117H mutant of human **butyrylcholinesterase** is able to catalyze the hydrolysis of organophosphate esters paraoxon and echothiophate. In order to understand this property, a mol. mechanic study of the mutant adduct was carried out. Each protonation site of H117 were examd. Results from mol. dynamics and quantum calcns. led us to propose two different mechanisms of hydrolysis depending on the protonation state of the mutated histidine.

L6 ANSWER 37 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:131854 HCAPLUS
DOCUMENT NUMBER: 128:280192
TITLE: The role of alanine 328 in substrate activation and binding of inhibitors to **butyrylcholinesterase**
AUTHOR(S): Saxena, Ashima; Redman, Ann M. G.; Qian, Naifeng; **Lockridge, Oksana**; Doctor, B. P.
CORPORATE SOURCE: Division of Biochemistry, Walter Reed Army Institute of Research, Washington, DC, 20307-5100, USA
SOURCE: Medical Defense Bioscience Review, Proceedings, Baltimore, May 12-16, 1996 (1996), Volume 1, 303-312. National Technical Information Service: Springfield, Va.
CODEN: 64UTAN
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Six of the fourteen arom. amino acid residues lining the gorge of **acetylcholinesterases** (AChE) are replaced by aliph. amino acid residues in **butyrylcholinesterases** (BChE). In particular, Tyr337(330) in mammalian AChE, which is replaced by Ala328(330) in human BChE, is implicated in the binding of ligands such as huperzine A, edrophonium, acridines, and one end of bisquaternary compds. such as BW284C51 and decamethonium. Tyr337 destabilizes the binding of phenothiazines such as ethopropazine, which contains a bulky exocyclic substitution. Inhibition studies of (-) huperzine A with human BChE mutants, where Ala328 (KI = 194.6 .mu.M) was modified to either Phe (Torpedo AchE; KI = 0.6 .mu.M) or Tyr (mammalian AChE; KI = 0.032 .mu.M),

have confirmed observations made with AChE mutants. However, inhibition of these mutants by ethopropazine (KI = 0.82 and 0.24 .mu.M) was not significantly different from that of wild-type BChE (KI = 0.18 .mu.M), suggesting that, besides Ala328, there were other amino acid residues responsible for the binding of ethopropazine. Docking of ethopropazine into the active-site gorge of human BChE and energy minimization of the complex revealed that ethopropazine appears to interact significantly with Ala328(Phe330), Gln119(Tyr121) and Val288(Phe290). The Ala328 mutants were different from wild-type BChE in that they did not display the phenomenon of substrate activation.

L6 ANSWER 38 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:130170 HCAPLUS
DOCUMENT NUMBER: 128:280089
TITLE: Human **butyrylcholinesterase** mutant, G117H, hydrolyzes echothiopate and paraoxon
AUTHOR(S): **Lockridge, O.**; Blong, R. M.; Froment, M.-T.; Masson, P.; Millard, C. B.; Broomfield, C. A.
CORPORATE SOURCE: Univ. Nebraska Medical Center, Omaha, NE, USA
SOURCE: Medical Defense Bioscience Review, Proceedings, Baltimore, May 12-16, 1996 (1996), Volume 1, 61-70. National Technical Information Service: Springfield, Va.
CODEN: 64UTAN
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Substitution of Gly117 with His to make the G117H mutant endowed human **butyrylcholinesterase** with the ability to hydrolyze organophosphate esters. The idea to make G117H came from C.A. Broomfield (Millard et al. Biochem. 1995, 34: 15925-15933), from his understanding of the catalytic mechanism. G117H was still able to hydrolyze butyrylthiocholine, benzoylcholine, and o-nitrophenylbutyrate, but in addn. it had acquired the ability to hydrolyze the antiglaucoma drug echothiopate and the pesticide paraoxon. Wild-type **butyrylcholinesterase** was irreversibly inhibited by echothiopate and paraoxon but G117H regained 100% activity within 2-3 min following reaction with these compds. On a polyacrylamide gel the same bands that stained for activity with butyrylthiocholine also stained for activity with echothiopate. G117H is the only enzyme known that hydrolyzes echothiopate. The G117H mutant was made by the polymerase chain reaction and expressed in Chinese Hamster Ovary cells. Echothiopate and paraoxon were hydrolyzed with the same kcat of 0.75 min-1. The half-life of the diethoxyphosphorylated intermediate of G117H was 0.5 min and of wild-type was 32 days. This calcs. to a rate acceleration of 100,000 for hydrolysis of echothiopate and paraoxon by the G117H mutant of **butyrylcholinesterase**.

L6 ANSWER 39 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:130078 HCAPLUS
DOCUMENT NUMBER: 128:280045
TITLE: Protein engineering of a human enzyme that hydrolyzes V and G nerve agents: design, construction and characterization
AUTHOR(S): Broomfield, Clarence A.; **Lockridge, Oksana**; Millard, Charles B.
CORPORATE SOURCE: U.S. Army Medical Research Institute of Chemical Defense, MD, 21010-5425, USA
SOURCE: Medical Defense Bioscience Review, Proceedings, Baltimore, May 12-16, 1996 (1996), Volume 1, 53-59. National Technical Information Service: Springfield,

Va.
CODEN: 64UTAN
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The goal of this research is to develop an enzyme of human origin that is capable of catalyzing the rapid hydrolysis of all of the nerve agents. This enzyme would be administered or induced in soldiers at risk of exposure to nerve agents as a pretreatment without undesired side effects. The feasibility of this type of protection has been well demonstrated with exogenous, stoichiometric scavengers and with bacterial enzymes, but no human enzyme is known that possesses the appropriate characteristics to be practical. We have made a beginning to the soln. of this problem by protein engineering of human **butyrylcholinesterase** (BuChE). Our first successful new enzyme, G117H, catalyzes the hydrolysis of GB, VX and DFP. When a second mutation was introduced at position 197 (G117H/E197Q) the hydrolysis of GD also was catalyzed. These new enzymes are not yet efficient enough to be used as biol. scavengers, but they provide conceptual validation and direction for continued rational design of the desired activity.

L6 ANSWER 40 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:794339 HCAPLUS
DOCUMENT NUMBER: 128:112287
TITLE: Organophosphorus Acid Anhydride Hydrolase Activity in Human **Butyrylcholinesterase**: Synergy Results in a Somanase
AUTHOR(S): Millard, Charles B.; **Lockridge, Oksana**; Broomfield, Clarence A.
CORPORATE SOURCE: United States Army Medical Research Institute of Chemical Defense, Aberdeen Proving Ground, MD, 21010-5425, USA
SOURCE: Biochemistry (1998), 37(1), 237-247
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Organophosphorus acid anhydride (OP) "nerve agents" are rapid, stoichiometric, and essentially irreversible inhibitors of serine hydrolases. By placing a His near the oxyanion hole of human **butyrylcholinesterase** (BChE), we made an esterase (G117H) that catalyzed the hydrolysis of several OP, including sarin and VX [Millard et al. (1995) Biochem. 34, 15925-15930]. G117H was limited, however, because it was irreversibly inhibited by pinacolyl methylphosphonofluoridate (soman); soman is among the most toxic synthetic poisons known. This limitation of G117H has been overcome by a new BChE (G117H/E197Q) that combines two engineered features: spontaneous dephosphonylation and slow aging (dealkylation). G117H/E197Q was compared with the single mutants BChE G117H and E197Q. Each retained **cholinesterase** activity with butyrylthiocholine as substrate, although kcat/Km decreased 11-, 11- or 110-fold for purified G117H, E197Q, or G117H/E197Q, resp., as compared with wild-type BChE. Only G117H/E197Q catalyzed soman hydrolysis; all four soman stereoisomers as well as sarin and VX were substrates. Phosphonylation and dephosphonylation reactions were stereospecific. Double mutant thermodn. cycles suggested that the effects of the His and Gln substitutions on phosphonylation were additive for PSCR or PRCR soman, but were cooperative for the PSCS stereoisomer. Dephosphonylation limited overall OP hydrolysis with apparent rate consts. of 0.006, 0.077, and 0.128 min-1 for the PR/SCR, PSCS, and PRCS soman stereoisomers, resp., at pH 7.5, 25.degree.. We conclude that synergistic protein design converted an archetypal "irreversible inhibitor" into a slow substrate for the

target enzyme.

L6 ANSWER 41 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:762607 HCAPLUS
DOCUMENT NUMBER: 128:45226
TITLE: Tetramerization domain of human **butyrylcholinesterase** is at the C-terminus
AUTHOR(S): Blong, Renee M.; Bedows, Elliott; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute and Dep. of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Omaha, NE, 68198-6805, USA
SOURCE: Biochemical Journal (1997), 327(3), 747-757
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Butyrylcholinesterase** (BChE) in human blood serum consists predominantly of tetramers. Recombinant BChE, however, expressed in CHO cells, consists of approx. 55% dimers, 10-30% tetramers, and 15-40% monomers. To det. the origin of the monomer species, the authors added the FLAG epitope (epitope tag; amino acid sequence DYKDDDDK) to the C-terminus of the enzyme, and expressed BChE-FLAG in CHO cells. It was found that secreted, active monomers had lost their FLAG epitope, suggesting that the monomers were made by proteolysis of dimers or tetramers at the C-terminus. To est. the no. of amino acids that could be deleted from the C-terminus without losing BChE activity, the authors expressed deletion mutants. It was found that deletion of .ltoreq.50 amino acids from the C-terminus yielded active monomers, but that deletion of 51 amino acids destroyed BChE activity and caused the inactive protein to remain within the cell. Deletion of .gtoreq.8 amino acids from the N-terminus also resulted in inactive protein that remained inside the cell. Monomeric BChE had wild-type Km and kcat values of 8 .mu.M and 2400 min-1, resp., for butyrylthiocholine, and showed substrate activation. The C571A mutant, although incapable of forming the interchain disulfide bond, had nearly the same amt. of tetrameric BChE as recombinant wild-type BChE. These results supported the conclusion that the tetramerization domain of BChE is at the C-terminus, within the terminal 50 amino acids, and that the interchain disulfide bond is not essential for tetramerization. Mol. modeling suggested that the tetramerization domain was a 4-helix bundle, stabilized by interactions of 7 conserved arom. amino acids.

L6 ANSWER 42 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:720338 HCAPLUS
DOCUMENT NUMBER: 127:328213
TITLE: Differences in Active Site Gorge Dimensions of **Cholinesterases** Revealed by Binding of Inhibitors to Human **Butyrylcholinesterase**
AUTHOR(S): Saxena, Ashima; Redman, Ann M. G.; Jiang, Xuliang; **Lockridge, Oksana**; Doctor, B. P.
CORPORATE SOURCE: Division of Biochemistry, Walter Reed Army Institute of Research, Washington, DC, 20307, USA
SOURCE: Biochemistry (1997), 36(48), 14642-14651
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Amino acid sequence alignments of **cholinesterases** revealed that 6 of 14 arom. amino acid residues lining the active center gorge of

acetylcholinesterase are replaced by aliph. amino acid residues in **butyrylcholinesterase**. The Y337(F330) in mammalian **acetylcholinesterase**, which is replaced by A328 in human **butyrylcholinesterase**, is implicated in the binding of ligands such as huperzine A, edrophonium, and acridines and one end of bisquaternary compds. such as BW284C51 and decamethonium. Y337 may sterically hinder the binding of phenothiazines such as ethopropazine, which contains a bulky exocyclic substitution. Inhibition studies of (-)-huperzine A with human **butyrylcholinesterase** mutants, where A328 (KI = 194.6 .mu.M) was modified to either F (KI = 0.6 .mu.M, as in Torpedo **acetylcholinesterase**) or Y (KI = 0.032 .mu.M, as in mammalian **acetylcholinesterase**), confirmed previous observations made with **acetylcholinesterase** mutants that this residue is important for binding huperzine A. Inhibition studies of ethopropazine with **butyrylcholinesterase** mutants, where A328 (KI = 0.18 .mu.M) was modified to either F (KI = 0.82 .mu.M) or Y (KI = 0.28 .mu.M), suggested that A328 was not solely responsible for the selectivity of ethopropazine. Vol. calcns. for the active site gorge showed that the poor inhibitory activity of ethopropazine toward **acetylcholinesterase** was due to the smaller dimension of the active site gorge, which was unable to accommodate the bulky inhibitor mol. The vol. of the **butyrylcholinesterase** active site gorge is .apprx.200 .ANG.3 larger than that of the **acetylcholinesterase** gorge, which allows the accommodation of ethopropazine in two different orientations as demonstrated by rigid-body refinement and mol. dynamics calcns.

L6 ANSWER 43 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:709533 HCAPLUS
DOCUMENT NUMBER: 128:45211
TITLE: Aging of di-isopropyl-phosphorylated human **butyrylcholinesterase**
AUTHOR(S): Masson, Patrick; Fortier, Pierre-Louis; Albaret, Christine; Froment, Marie-Therese; Bartels, Cynthia F.; **Lockridge, Oksana**
CORPORATE SOURCE: Cent. Rech. Ser. Sante Armees, Unite Biochimie, La Tronche, 38702, Fr.
SOURCE: Biochemical Journal (1997), 327(2), 601-607
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Organophosphate-inhibited **cholinesterases** can be reactivated by nucleophilic compds. Sometimes phosphylated (phosphorylated or phosphonylated) **cholinesterases** become progressively refractory to reactivation; this can result from different reactions. The most frequent process, termed 'aging', involves the dealkylation of an alkoxy group on the phosphyl moiety through a carbocation mechanism. In attempting to det. the amino acid residues involved in the aging of **butyrylcholinesterase** (BuChE), the human BuChE gene was mutated at several positions corresponding to residues located at the rim of the active site gorge and in the vicinity of the active site. Mutant enzymes were expressed in Chinese hamster ovary cells. Wild-type BuChE and mutants were inhibited by di-iso-Pr fluorophosphate at pH 8.0 and 25.degree.. Di-isopropyl-phosphorylated enzymes were incubated with the nucleophilic oxime 2-pyridine aldoxime methiodid and their reactivatability was detd. Reactivatability was expressed by the first-order rate const. of aging and/or the half-life of aging (t 1/2). The t 1/2 was found to be of the order of 60 min for wild-type BuChE. Mutations on Glu-197 increased t 1/2 60-fold. Mutation W82A increased t

1/2 13-fold. Mutation D70G increased t 1/2 8-fold. Mutations in the vicinity of the active site serine residue had either moderate or no effect on aging; t 1/2 was doubled for F329C and F329A, increased only 4-fold for the double mutant A328G + F329S, and no change was obsd. for the A328G mutant, indicating that the isopropoxy chain to be dealkylated does not directly interact with Ala-328 and Phe-329. These results were interpreted by mol. modeling of di-isopropylphosphorylated wild-type and mutant enzymes. Mol. dynamics simulations indicated that the iso-Pr chain that is lost interacted with Trp-82, suggesting that Trp-82 has a role in stabilizing the carbonium ion that is released in the dealkylation step. This study emphasized the important role of the Glu-197 carboxylate in stabilizing the developing carbocation, and the allosteric control of the dealkylation reaction by Asp-70. Indeed, although Asp-70 does not interact with the phosphor6yl moiety, mutation D70G affects the rate of aging. This indirect control was interpreted in terms of change in the conformational state of Trp-82 owing to internal motions of the .OMEGA. loop (Cys-65-Cys-92) in the mutant enzyme.

L6 ANSWER 44 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:527192 HCAPLUS
DOCUMENT NUMBER: 127:157741
TITLE: In vitro pyridostigmine inhibition of red cell **acetylcholinesterase**: a comparison in Gulf War veterans and normal controls
AUTHOR(S): Gentry, Mary K.; Powell, Stephanie E.; Bitsko, Nancy; Bartels, Cynthis F.; Doctor, B. P.; Chung, Raymond C. Y.; **Lockridge, Oksana**; Ribas, Jorge L.; Roy, Michael J.
CORPORATE SOURCE: Division Biochemistry, Walter Reed Army Institute Research, Washington, DC, 20307, USA
SOURCE: Medical Defense Bioscience Review, Proceedings, Baltimore, May 12-16, 1996 (1996), Volume 3, 1254-1261. National Technical Information Service: Springfield, Va.
CODEN: 64UTAN
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Estd. reactivation times for red cell **acetylcholinesterase** after in vitro pyridostigmine inhibition were compared in blood samples from 20 veterans of Operation Desert Storm and 20 normal control subjects, matched for sex and age. All Gulf War veterans indicated they had taken pyridostigimine as a pretreatment drug for nerve agent exposure in Operation Desert Storm. **Acetylcholinesterase** was inhibited in whole blood lysates at pyridostigmine concns. from 1 to 7.5 .mu.M. **Butyrylcholinesterase** was specifically inhibited with iso-OMPA to prevent interference with detn. of **acetylcholinesterase** activity. Concns. of red cell **acetylcholinesterase** and plasma **butyrylcholinesterase** were detd. Mean whole blood **acetylcholinesterase** for all subjects was 5.7 U/mL .+-. 0.7; mean plasma **butyrylcholinesterase** was 4.9 U/mL .+-. 1.1. Mean spontaneous reactivation time (t1/2 at 2.5 .mu.M pyridostigmine) for all subjects was 42.6 min .+-. 5.4; mean for veterans = 43.2 .+-. 6.2; mean for controls = 42.1 .+-. 4.6. Statistical anal. of reactivation times (repeated measures ANOVA) revealed no statistically significant difference between controls and veterans, but there were significant differences ($p = 0.01$) between controls and veterans were not statistically significant although, again, there were significant differences between the sexes across both groups. Phenotyping of **butyrylcholinesterase** showed that all Gulf War veterans had the homozygous usual, wild-type allele. Examn. of kinetics of **acetylcholinesterase** inhibition and

butyrylcholinesterase concns. in this limited population revealed no indication of genetic predispositions that could result in adverse effects upon exposure to pyridostigmine.

L6 ANSWER 45 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:454116 HCAPLUS
DOCUMENT NUMBER: 127:201978
TITLE: Importance of aspartate-70 in organophosphate inhibition, oxime reactivation and aging of human **butyrylcholinesterase**
AUTHOR(S): Masson, Patrick; Froment, Marie-Therese; Bartels, Cynthia F.; **Lockridge, Oksana**
CORPORATE SOURCE: Unite de Biochimie, Centre de Recherches du Service de Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Biochemical Journal (1997), 325(1), 53-61
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Asp-70 is the defining amino acid in the peripheral anionic site of human **butyrylcholinesterase** (BuChE), whereas **acetylcholinesterase** has several addnl. amino acids, the most important one being Trp-277 (Trp-279 in Torpedo AChE). We studied mutants D70G, D70K and A277W to evaluate the role of Asp-70 and Trp-277 in reactions with organophosphates. We fond that Asp-70 was important for binding pos. charged echothiophate, but not neutral paraoxon and iso-OMPA. Asp-70 was also important for binding of pos. charged pralidoxime (2-PAM) and for activation of re-activation by excess 2-PAM. Excess 2-PAM had an effect similar to substrate activation, suggesting the binding of 2 mol of 2-PAM to wild-type but not to the D70G mutant. A surprising result was that Asp-70 was important for irreversible aging, the D70G mutant having a 3- and 8-fold lower rate of aging for paraoxon-inhibited and diisopropyl fluorophosphate-inhibited BuChE. Mutants of Asp-70 had the same rate consts. for phosphorylation and re-activation by 2-PAM as wild-type. The A277W mutant behaved like wild-type in all assays. Our results predict that people with the atypical (D70G) variant of BuChE will be more sensitive to the toxic effects of echothiophate, but will be equally sensitive to paraoxon and di-iso-Pr fluorophosphate. People with the D70G mutation will be resistant to re-activation of their inhibited BuChE by 2-PAM, but this will be offset by the lower rate of irreversible aging of inhibited BuChE, allowing some regeneration by spontaneous hydrolysis.

L6 ANSWER 46 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:400181 HCAPLUS
DOCUMENT NUMBER: 127:104939
TITLE: Insect larvae: a novel expression system for human **butyrylcholinesterase**
AUTHOR(S): Platteborze, Peter L.; Mellott, James D.; Broomfield, Clarence A.; **Lockridge, Oksana**
CORPORATE SOURCE: U.S. Army Medical Research Institute Chemical Defense, APG-EA, MD, 21010-5425, USA
SOURCE: Protein Engineering (1997), 10(Suppl.), 13
CODEN: PRENE9; ISSN: 0269-2139
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Recombinant baculovirus vectors expressing the human **butyrylcholinesterase** (BuChE) gene were administered to fourth instar cabbage looper (Trichoplusia ni) larvae by growing the larvae for .apprx.72 h on infected synthetic medium. Infected T. ni larvae

homogenate generated a significantly greater amt. of BuChE activity than transfected COS cells or Sf9 cells infected with recombinant baculovirus. Unlike COS cells or Sf9 cells, the T. ni larvae produced enough BuChE to assay for organophosphate hydrolysis activity, an important step in engineering BuChE to hydrolyze organophosphate chem. warfare nerve agents. Infected T. ni larvae could also serve as an animal model system for testing recombinant BuChE activity against chem. warfare nerve agents in vivo.

L6 ANSWER 47 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:195386 HCAPLUS
DOCUMENT NUMBER: 126:168374
TITLE: Role of aspartate 70 and tryptophan 82 in binding of succinyldithiocholine to human **butyrylcholinesterase**
AUTHOR(S): Masson, Patrick; Legrand, Pierre; Bartels, Cynthia F.; Froment, Marie-Therese; Schopfer, Lawrence M.; **Lockridge, Oksana**
CORPORATE SOURCE: Unite de Biochimie, Centre de Recherches du Service de Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Biochemistry (1997), 36(8), 2266-2277
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The atypical variant of human **butyrylcholinesterase** has Gly in place of Asp-70. Patients with this D70G mutation respond abnormally to the muscle relaxant, succinyldicholine, experiencing hours of apnea rather than the intended 3 min. Asp-70 is at the rim of the active site gorge 12 .ANG. from active site residue Ser-198. An unanswered question in the literature is why the atypical variant has a 10-fold increase in Km for compds. with a single pos. charge, but a 100-fold increase in Km for compds. with 2 pos. charges. Here, the authors mutated residues Asp-70, Trp-82, Trp-231, Glu-197, and Tyr-332 and expressed mutant enzymes in mammalian cells. Steady-state kinetic parameters for the hydrolysis of butyrylthiocholine, benzoylcholine, succinyldithiocholine, and o-nitrophenyl butyrate were detd. The wild-type and the D70G mutant enzymes had identical kcat values for all substrates. Mol. modeling and mol. dynamics suggested that succinyldicholine could bind in 2 consecutive orientations in the active site gorge; formation of one complex caused a conformational change in the omega loop involving Asp-70 and Trp-82. The authors propose the formation of 3 enzyme-substrate intermediates preceding the acyl-enzyme intermediate; kinetic data support this contention. Substrates with a single pos. charge interact with Asp-70 just once, whereas substrates with 2 pos. charges, e.g., succinyldithiocholine, interact with Asp-70 in 2 complexes, thus explaining the 10- and 100-fold increases in Km in the D70G mutant.

L6 ANSWER 48 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:26262 HCAPLUS
DOCUMENT NUMBER: 126:101090
TITLE: A single amino acid substitution, Gly117His, confers phosphotriesterase (organophosphorus acid anhydride hydrolase) activity on human **butyrylcholinesterase**
AUTHOR(S): **Lockridge, Oksana**; Blong, Renee M.; Masson, Patrick; Froment, Marie-Therese; Millard, Charles B.; Broomfield, Clarence A.
CORPORATE SOURCE: Eppley Institute and Department of Biochemistry and Molecular Biology, University of Nebraska Medical

Center, Omaha, NE, 8198-6805, USA
SOURCE: Biochemistry (1997), 36(4), 786-795
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The G117H mutant of human **butyrylcholinesterase** (EC 3.1.1.8) (I) was expressed in CHO cells. Substitution of Gly-117 with His to make the G117H mutant endowed I with the ability to catalyze the hydrolysis of organophosphate esters. G117H was still able to hydrolyze butyrylthiocholine, benzoylcholine, and o-nitrophenyl butyrate, but in addn. it had acquired the ability to hydrolyze the antiglaucoma drug, echothiophate, and the pesticide, paraoxon. Wild-type I was irreversibly inhibited by echothiophate and paraoxon, but G117H regained 100% activity within 2-3 min following reaction with these compds. On a polyacrylamide gel, the same bands that stained for activity with butyrylthiocholine also stained for activity with echothiophate. G117H is the only enzyme known that hydrolyzes echothiophate. Diethoxyphosphorylated G117H aged with a half-time of 5.5 h, a rate 600-fold slower than the rate of hydrolysis. Echothiophate and paraoxon were hydrolyzed with the same kcat of 0.75 min-1. This calcd. to a rate acceleration of 100 000-fold for hydrolysis of echothiophate and paraoxon by the G117H mutant compared to the nonenzymic rate.

L6 ANSWER 49 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:159570 HCAPLUS
DOCUMENT NUMBER: 124:254383
TITLE: Mutation of human **butyrylcholinesterase** glycine 117 to histidine preserves activity but confers resistance to organophosphorus inhibitors
AUTHOR(S): Broomfield, C. A.; Millard, C. B.; **Lockridge, O.**; Caviston, T. L.
CORPORATE SOURCE: Biochemical Pharmacology Branch, U.S. Army Medical Research Institute Chemical Defense, Aberdeen Proving Ground, MD, 21010-5425, USA
SOURCE: Enzymes of the Cholinesterase Family, [Proceedings of the International Meeting on Cholinesterases], 5th, Madras, Sept. 24-28, 1994 (1995), Meeting Date 1994, 169-75. Editor(s): Quinn, Daniel M. Plenum: New York, N. Y.
CODEN: 62LSAT
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Computer-aided modeling was used to identify mutation sites that potentially would produce an enzyme from **butyrylcholinesterase** that would catalyze rapid hydrolysis of organophosphorus inhibitors. Two mutants (G117H and G121H) were created and expressed to test the models. Replacement of glycine-121 with histidine eliminated activity, probably due to steric interference with substrate binding. Replacement of glycine-117 with histidine, however, produced an enzyme that retained, for the most part, its ability to hydrolyze the normal substrates but was highly resistant to inhibition by organophosphorus inhibitors. Furthermore, once an organophosphorus inhibitor reacted with the G117H mutant, reactivation was much more rapid than in the wild-type enzyme, resulting in actual turnover of the organophosphorus compd.

L6 ANSWER 50 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:159553 HCAPLUS
DOCUMENT NUMBER: 124:221804
TITLE: **Butyrylcholinesterase** transcription start

site and promoter
AUTHOR(S): Jbilo, Omar; Toutant, Jean-Pierre; Chatonnet, Arnaud; **Lockridge, Oksana**
CORPORATE SOURCE: INRA, Montpellier, 34060, Fr.
SOURCE: Enzymes of the Cholinesterase Family, [Proceedings of the International Meeting on Cholinesterases], 5th, Madras, Sept. 24-28, 1994 (1995), Meeting Date 1994, 23-8. Editor(s): Quinn, Daniel M. Plenum: New York, N. Y.
CODEN: 62LSAT
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A review with 12 refs.

L6 ANSWER 51 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:83200 HCAPLUS
DOCUMENT NUMBER: 124:254360
TITLE: Asp70 in the peripheral anionic site of human **butyrylcholinesterase**
AUTHOR(S): Masson, Patrick; Froment, Marie-Therese; Bartels, Cynthia F.; **Lockridge, Oksana**
CORPORATE SOURCE: Unite de Biochimie, Centre de Recherches du Service de Sante des Armees, La Tronche, Fr.
SOURCE: European Journal of Biochemistry (1996), 235(1/2), 36-48
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Springer
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The amino acids at the mouth of the active site gorge was detd. important for the function of human **butyrylcholinesterase**. Mutants D70G, Q119Y, G283D, A277W, A277H, and A277W/G283D were expressed in human embryonal kidney cells and the secreted enzymes were assayed by steady-state kinetics. Only 1 amino acid, D70 was important for function. When D70 was mutated to G, the same mutation as in the naturally occurring atypical **butyrylcholinesterase**, the affinity for pos. charged substrates and pos. charged inhibitors decreased 5-30-fold. The D70G mutant had another striking abnormality in that it was virtually devoid of the phenomenon of substrate activation by excess butyrylthiocholine. Thus, though kcat was the same for wild-type and D70G mutant, being 24000 min-1 at low butyrylthiocholine concns. (0.01-01 mM), it failed to increase for the D70G mutant at 40 mM butyrylthiocholine, whereas it increased threefold for wild type. The D70G mutant was more sensitive to changes in salt concn., its catalytic rate decreasing more than that of the wild type. The D70G mutant appeared to have a greater surface neg. charge than wild type suggesting that the D70G mutant had a conformation different from that of the wild type. That D70 affects the function of **butyrylcholinesterase**, together with its location at the mouth of the active-site gorge, supports the hypothesis that D70 is a component of the peripheral anionic site of **butyrylcholinesterase**. Mutants contg. arom. amino acids at the mouth of the gorge had increased binding affinity for propidium and fasciculin, but unaltered function, suggesting that arom. amino acids are not important to the function of the peripheral anionic site of **butyrylcholinesterase**.

L6 ANSWER 52 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1995:945137 HCAPLUS
DOCUMENT NUMBER: 123:333693
TITLE: Design and expression of organophosphorus acid anhydride hydrolase activity in human

butyrylcholinesterase
AUTHOR(S): Millard, Charles B.; **Lockridge, Oksana**; Broomfield, Clarence A.
CORPORATE SOURCE: United States Army Medical Research Institute of Chemical Defense, Aberdeen Proving Ground, MD, 21010-5425, USA
SOURCE: Biochemistry (1995), 34(49), 15925-33
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Serine esterases and proteases are rapidly and irreversibly inhibited by organophosphorus (OP) nerve agents. To overcome this limitation, we selected several residues that were predicted to be within 3-10 .ANG. of both the active site Ser O.gamma. and the oxyanion hole of human **butyrylcholinesterase** (BuChE) for mutation to His (G115H, G117H, Q119H, and G121H). In marked contrast with wild-type (WT) and all other His mutants tested, G117H underwent spontaneous reactivation following OP inhibition to regain 100% of original esterase activity with max. k3 values of approx. 6.8 .times. 10-5 and 16 .times. 10-5 s-1 for GB (sarin) and VX, resp., in 0.1M Bis-Tris, 25.degree.. The free energy of activation for k3 was 19 kcal/mol, and measurement of pH dependence suggested that reactivation resulted from an acidic group with a pKa of 6.2. To evaluate further the importance of His in achieving this result, the authors changed the same Gly to Lys (G117K) and compared its substrate and inhibitor kinetics with those of G117H. Both mutants retained esterase activity with Km values similar to those of WT for neutral ester hydrolysis, but G117K did not reactivate. Complete reactivation proved that G117H is not irreversibly inhibited but instead functions as a catalyst for OP hydrolysis. Dephosphonylation is the rate-limiting step, and G117H effects overall rate const. enhancements of approx. 100- and 2000-fold above the uncatalyzed hydrolysis of GB and VX, resp., at pH 6.0, 25.0 .degree.. It was concluded that an appropriately positioned imidazolium ion in the oxyanion hole catalyzes dephosphonylation and, thereby, confers a novel organophosphorus acid anhydride hydrolase (diisopropylfluorophosphatase) activity upon BuChE.

L6 ANSWER 53 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1995:235846 HCAPLUS
DOCUMENT NUMBER: 122:236504
TITLE: Endogenous **butyrylcholinesterase** in SV40 transformed cell lines: COS-1, COS-7, MRC-5 SV40, and WI-38 VA13
AUTHOR(S): Kris, Morena; Jbilo, Omar; Bartels, Cynthia F.; Masson, Patrick; Rhode, Solon; **Lockridge, Oksana**
CORPORATE SOURCE: Eppley Institute, University of Nebraska Medical Center, Omaha, NE, 68198, USA
SOURCE: In Vitro Cellular & Developmental Biology: Animal (1994), 30A(10), 680-9
CODEN: IVCAED; ISSN: 1071-2690
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Comparison of proteins expressed by SV40 transformed cell lines and untransformed cell lines is of interest because SV40 transformed cells are immortal, whereas untransformed cells senesce after about 50 doublings. In MRC-5 SV40 cells, only seven proteins have previously been reported to shift from undetectable to detectable after transformation by SV40 virus. The authors report that **butyrylcholinesterase** is an 8th protein in this category. **Butyrylcholinesterase** activity in transformed

MRC-5 SV40 cells increased at least 150-fold over its undetectable level in MRC-5 parental cells. Other SV40 transformed cell lines, including COS-1, COS-7, and WI-38 VA13, also expressed endogenous **butyrylcholinesterase**, whereas the parental, untransformed cell lines, CV-1 and WI-38, had no detectable **butyrylcholinesterase** activity or mRNA. Infection of CV-1 cells by SV40 virus did not result in expression of **butyrylcholinesterase**, showing that the **butyrylcholinesterase** promoter was not activated by the large T antigen of SV40. Thus, **butyrylcholinesterase** expression resulted from events related to cell immortalization and did not result from activation by the large T antigen.

L6 ANSWER 54 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1995:207130 HCAPLUS
DOCUMENT NUMBER: 122:6206
TITLE: Tissue distribution of human **acetylcholinesterase** and **butyrylcholinesterase** messenger RNA
AUTHOR(S): Jbilo, Omar; Bartels, Cynthia F.; Chatonnet, Arnaud; Toutant, Jean-Pierre; **Lockridge, Oksana**
CORPORATE SOURCE: Inst. Natl. Rech. Agron., Physiol. Animale 9, Montpellier, 34060, Fr.
SOURCE: Toxicon (1994), 32(11), 1445-57
CODEN: TOXIA6; ISSN: 0041-0101
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Cholinesterase** inhibitors are known to occur naturally in the calabar bean (eserine), green potatoes (solanine), insect-resistant crab apples, the coca plant (cocaine) and snake venom (fasciculin). There are also synthetic **cholinesterase** inhibitors, for example man-made insecticides. These inhibitors are known to inactivate **acetylcholinesterase** and **butyrylcholinesterase** as well as other targets. From a study of the tissue distribution of **acetylcholinesterase** and **butyrylcholinesterase** mRNA by Northern blot anal., the authors have found the highest levels of **butyrylcholinesterase** mRNA in the liver and lungs, tissues known as the principal detoxication sites of the human body. These results indicate that **butyrylcholinesterase** may be a first line of defense against poisons that are eaten or inhaled.

L6 ANSWER 55 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:673417 HCAPLUS
DOCUMENT NUMBER: 121:273417
TITLE: Promoter and transcription start site of human and rabbit **butyrylcholinesterase** genes
AUTHOR(S): Jbilo, Omar; Toutant, Jean-Pierre; Vatsis, Kostas P.; Chatonnet, Arnaud; **Lockridge, Oksana**
CORPORATE SOURCE: Inst. Natl. Recherche Agronomique, Montpellier, 34060, Fr.
SOURCE: Journal of Biological Chemistry (1994), 269(33), 20829-37
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Two kilobase segments of the 5'-untranslated regions of the human and rabbit **butyrylcholinesterase** (BCHE) genes were characterized. The sequences shared extensive identity except for a 333-base pair (bp) Alu repeat present only in human BCHE. One single transcription start site was found in both genes with the techniques of primer extension,

amplification of the 5'-end of mRNA, and RNase protection. Cap sites in human and rabbit BCHE genes were found in strictly homologous positions. In human BCHE, the transcription start site was found 157 bp upstream of Met-28, the translation start site. Potential regulatory elements in both promoters included one AP1 site and multiple sites for topoisomerase, Oct-1 and PEA-3. Transient expression of BCHE-reporter gene constructs showed that a 194-bp fragment of the 5'-flanking region of human BCHE and a 570-bp fragment of rabbit BCHE were sufficient for promoting chloramphenicol acetyltransferase activity in HeLa cells. No consensus TATA and CAAT boxes were found. However, the sequence around the transcription start site exhibited homol. with initiator elements found in other TATA-less promoters in developmentally regulated genes.

L6 ANSWER 56 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:474729 HCAPLUS
DOCUMENT NUMBER: 121:74729
TITLE: Expression of recombinant **butyrylcholinesterase** in mammalian cells
AUTHOR(S): **Lockridge, O.**
CORPORATE SOURCE: Med. Cent., Nebraska Univ., Omaha, NE, USA
SOURCE: Report (1992), Order No. AD-A262582, 95 pp. Avail.: NTIS
From: Gov. Rep. Announce. Index (U. S.) 1993, 93(14), Abstr. No. 341,805
DOCUMENT TYPE: Report
LANGUAGE: English
AB Sequencing of the **acetylcholinesterase** gene from 55 human subjects showed that the red blood cell **acetylcholinesterase** was identical to the YT blood group antigen. The common YT1 blood group had His-322 and the rare YT2 blood group had Asn-322. The human **butyrylcholinesterase** and its mutants were also expressed in recombinant CHO cells.

L6 ANSWER 57 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:534140 HCAPLUS
DOCUMENT NUMBER: 119:134140
TITLE: Recombinant human **butyrylcholinesterase** G390V, the fluoride-2 variant, expressed in Chinese hamster ovary cells, is a low affinity variant
AUTHOR(S): Masson, Patrick; Adkins, Steve; Gouet, Patrice; **Lockridge, Oksana**
CORPORATE SOURCE: Unite Biochim., Cent. Rech. Serv. Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Journal of Biological Chemistry (1993), 268(19), 14329-41
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The kinetics of a recombinant fluoride-2 variant of human **butyrylcholinesterase** (contg. a Gly390.fwdarw.Val mutation) secreted by Chinese hamster ovary cells were compared to recombinant wild-type enzyme and to wild-type **butyrylcholinesterase** purified from human plasma, where wild-type refers to the most commonly obsd. form of the enzyme. The wild-type and fluoride-2-variant enzymes were indistinguishable with regard to hydrolysis of benzoylcholine (Km = 5 .mu.M), neutral esters, and at high concns. of acetylthiocholine, propionylthiocholine, and butyrylthiocholine. However, at low substrate concns., Km values for acetylthiocholine and succinyldithiocholine were 2-6-fold higher for the fluoride-2-variant. The pH rate profiles revealed small differences in pK.alpha. that could be attributed to changes in the

active site histidine environment. On the other hand, Arrhenius plot anal. of o-nitrophenylbutyrate hydrolysis at pH 7.5 showed no difference in activation energy between fluoride-2 and wild-type **butyrylcholinesterases**. Both exhibited an anomalous temp. dependence with a wavelike change in activation energy around 18 .degree.C. Affinity of the fluoride-2 variant for sodium fluoride, tacrine, dibucaine, amodiaquin, and succinyldicholine was lower than for wild-type enzyme. Apparent Ki for succinyldicholine was 125 .mu.M for the fluoride-2 variant and 20 .mu.M for the wild-type enzyme. Organophosphate inhibition showed equiv. reactivity, indicating that the point mutation altered only the binding properties of the variant. Thus, Km and Ki changes explain the succinyldicholine sensitivity of people carrying the fluoride-2 variant.

L6 ANSWER 58 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:231359 HCAPLUS
DOCUMENT NUMBER: 118:231359
TITLE: Genetic variant of human **acetylcholinesterase**. SV-40 transformed cell lines, for example COS-1, but not parental untransformed cell lines, express **butyrylcholinesterase** (BCHE)
AUTHOR(S): **Lockridge, Oksana**; Bartels, Cynthia F.; Zelinski, Teresa; Jbilo, Omar; Kris, Morena
CORPORATE SOURCE: Eppley Inst., Univ. Nebraska, Omaha, NE, 68198-6805, USA
SOURCE: Multidiscip. Approaches Cholinesterase Funct., [Proc. OHOLO Conf.], 36th (1992), 53-9. Editor(s): Shafferman, Avigdor; Velan, Baruch. Plenum: New York, N. Y.
CODEN: 58ZCAE
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Until now no genetic variant of human **acetylcholinesterase** has been reported. This enzyme is considered essential to life and it was thought that genetic variants of acetylcholinestease were incompatible with life. However, we have found a common polymorphism in human acetylcholinestease, histidine 322 being changed to asparagine, in 5% of ACHe alleles of European and American populations. Furthermore, this genetic variation is assocd. with the YT blood group. We conclude that the YT blood group antigen is located on red blood cell **acetylcholinesterase**. The literature shows only one cultured cell line that has BChE activity, the HuH-7 hepatoma cell line (Hada et al., 1987). We have found that SV40 transformed cell lines including COS-1 and COS-7 monkey kidney cell lines, and WI38 VA13 and MRC-5 SV40 human lung embryonal cells have significant levels of BChE both in the cell lyase and secreted into the culture medium. In contrast, the nontransformed parental cell lines CV-1, W138, and MRC-5 have little or no BChE.

L6 ANSWER 59 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:225377 HCAPLUS
DOCUMENT NUMBER: 118:225377
TITLE: Identification of two different point mutations associated with the fluoride-resistant phenotype for human **butyrylcholinesterase**
AUTHOR(S): Nogueira, Christine P.; Bartels, Cynthia F.; McGuire, Mary C.; Adkins, Steve; Lubrano, Tina; Rubinstein, Herbert M.; Lightstone, Harold; Van der Spek, Abraham F. L.; **Lockridge, Oksana**; La Du, Bert N.
CORPORATE SOURCE: Med. Sch., Univ. Michigan, Ann Arbor, MI, 48109-0572, USA

SOURCE: American Journal of Human Genetics (1992), 51(4), 821-8
CODEN: AJHGAG; ISSN: 0002-9297
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fluoride variant of human **butyrylcholinesterase** owes its name to the observation that it is resistant to inhibition by 0.050 mM sodium fluoride in the in vitro assay. Individuals who are heterozygous for the fluoride and atypical alleles experience about 30 min of apnea, rather than the usual 3-5 min, after receiving succinyldicholine. Earlier we reported that the atypical variant has a nucleotide substitution which changes Asp 70 to Gly. In the present work we have identified two different point mutations assocd. with the fluoride-resistant phenotype. Fluoride-1 has a nucleotide substitution which changes Thr 243 to Met (ACG to ATG). Fluoride-2 has a substitution which changes Gly 390 to Val (GGT to GTT). These results were obtained by DNA sequence anal. of the **butyrylcholinesterase** gene after amplification by PCR. The subjects for these analyses were 4 patients and 21 family members.

L6 ANSWER 60 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:186898 HCAPLUS
DOCUMENT NUMBER: 118:186898
TITLE: Expression and refolding of functional human **butyrylcholinesterase** from E. coli
AUTHOR(S): Masson, Patrick; Adkins, Steve; Pham-Trong, Philippe; **Lockridge, Oksana**
CORPORATE SOURCE: Cent. Rech., Serv. Sante des Armees, La Tronche, 38702, Fr.
SOURCE: Multidiscip. Approaches Cholinesterase Funct., [Proc. OHOLO Conf.], 36th (1992), 49-52. Editor(s): Shafferman, Avigdor; Velan, Baruch. Plenum: New York, N. Y.
CODEN: 58ZCAE
DOCUMENT TYPE: Conference
LANGUAGE: English

AB Recombinant human **butyrylcholinesterase** (BuChE) can be produced in Escherichia coli and renatured to generate the active tetramer. However, for practical interest, the conditions of refolding have to be optimized. Nevertheless, 2 conclusions can be drawn: (a) sugars are not essential for BuChE activity (but sugars are important for biol. stability and circulatory lifetime of the plasma enzyme since they protect it against proteases); (b) though BuChE is a disulfide-linked dimer of dimers composed of 3-disulfide looped single domain subunits, its folding to the functionally active state is thermodynamically controlled.

L6 ANSWER 61 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:544602 HCAPLUS
DOCUMENT NUMBER: 117:144602
TITLE: Structure of human **butyrylcholinesterase** gene and expression in mammalian cells
AUTHOR(S): **Lockridge, Oksana**; La Du, Bert N.
CORPORATE SOURCE: Med. Sch., Univ. Michigan, Ann Arbor, MI, 48109-0626, USA
SOURCE: Cholinesterases Proc. Int. Meet. Cholinesterases, 3rd (1991), Meeting Date 1990, 168-71. Editor(s): Massoulie, Jean. Am. Chem. Soc.: Washington, D. C.
CODEN: 57VWAD
DOCUMENT TYPE: Conference
LANGUAGE: English

AB Single copy genes are very important for the Human Genome Mapping and

Sequencing Project because they are used as landmarks to define position on the phys. map. **Butyrylcholinesterase** (BCHE) is a single copy gene in the human genome as well as in order vertebrates. The authors have detd. the structure of the human gene and have recovered the gene by PCR from genomic DNA of approx. 100 individuals. PCR and DNA sequencing were used to identify nucleotide substitutions in the rare genetic variants of human BChE assocd. with an abnormal response to the muscle relaxant succinylcholine. When human cDNA was expressed in CHO cells >95% of activity was secreted as a tetrameric BChE having normal substrate and inhibitor specificities.

L6 ANSWER 62 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:484472 HCAPLUS
DOCUMENT NUMBER: 117:84472
TITLE: DNA mutation associated with the human **butyrylcholinesterase** K-variant and its linkage to the atypical variant mutation and other polymorphic sites
AUTHOR(S): Bartels, C. F.; Jensen, F. S.; **Lockridge, O.** ; Van der Spek, A. F. L.; Rubinstein, H. M.; Lubrano, T.; La Du, B. N.
CORPORATE SOURCE: Sch. Med., Univ. Michigan, Ann Arbor, MI, USA
SOURCE: American Journal of Human Genetics (1992), 50(5), 1086-103
CODEN: AJHGAG; ISSN: 0002-9297
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Genomic DNA from two families exhibiting the K-variant phenotype of serum **butyrylcholinesterase** was amplified by PCR and sequenced to det. the mol. basis of this variant. The K-variant phenotype was found to be assocd. with a DNA transition from guanine to adenine at nucleotide 1615, which caused an amino acid change from alanine 539 to threonine (GCA.fwdarw.ACA; Ala539.fwdarw.Thr). There was a 30% redn. of serum **butyrylcholinesterase** activity assocd. with this mutation. Amplification and sequencing of DNA from a random sample of 47 unrelated people gave a frequency of .128 for the K-variant allele. Thus, 1 person in 63 should be homozygous for the K-variant, making the K-variant the most common **butyrylcholinesterase** variant. The K-variant mutation was also found to be present in 17 (89%) of 19 **butyrylcholinesterase** genes contg. the point mutation which causes the atypical phenotype of **butyrylcholinesterase** (GAT.fwdarw.GGT; Asp70.fwdarw.Gly). The presence of the K-variant in the same mol. as the atypical variant does not contribute to the qual. change in the atypical enzyme, but it most likely accounts for the approx. one-third redn. in Vmax of **butyrylcholinesterase** activity in atypical serum. Two addnl. point mutations located in noncoding regions of the gene were also obsd. to be in linkage disequil. with the K-variant mutation. As many as four different point mutations have been identified within a single **butyrylcholinesterase** gene. Inhibition tests of the enzyme in plasma are usually used to distinguish the K-variant from the usual enzyme when the former is present with the heterozygous atypical variant (AK phenotype vs. UA phenotype). Inhibition tests were performed on plasma enzyme from the four possible genotypic combinations of the heterozygous atypical mutation with or without the K-variant mutation on either allele; it was found that the AK phenotype was caused by three genotypes (A/K, AK/K, and U/A) and that the UA phenotype was caused by two genotypes (U/A and U/AK).

L6 ANSWER 63 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:52665 HCAPLUS

DOCUMENT NUMBER: 116:52665
TITLE: The cloned **butyrylcholinesterase** (BCHE) gene maps to a single chromosome site, 3q26
AUTHOR(S): Allderdice, P. W.; Gardner, H. A. R.; Galutira, D.; **Lockridge, O.**; LaDu, B. N.; McAlpine, P. J.
CORPORATE SOURCE: Fac. Med., Mem. Univ. Newfoundland, St. John's, NF, A1B 3V6, Can.
SOURCE: Genomics (1991), 11(2), 452-4
CODEN: GNMCEP; ISSN: 0888-7543
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Human tissues have 2 distinct **cholinesterase** activities: **acetylcholinesterase** and **butyrylcholinesterase**. **Acetylcholinesterase** functions in the transmission of nerve impulses, whereas the physiol. function of **butyrylcholinesterase** remains unknown. An atypical form of **butyrylcholinesterase** or the absence of its activity leads to prolonged apnea following administration of the muscle relaxant suxamethonium. Inheritance of these **butyrylcholinesterase** variants is consistent with the enzyme activity being encoded in a single autosomal locus, BCHE (formerly CHE1 and E1), which has been assigned to chromosome 3. Previous in situ hybridization of a BCHE cDNA probe gave evidence of homologous sequences at 3q26, and 16q11-q23, raising the possibility of more than 1 locus coding for **butyrylcholinesterase** (Soreq, H., et al., 1987). Using a different cDNA probe hybridized in situ to 46,XX,inv(3)(p25q21) metaphase chromosomes, the localization of BCHE to a single autosomal location, 3q26, is reported.

L6 ANSWER 64 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:35266 HCAPLUS
DOCUMENT NUMBER: 116:35266
TITLE: Human **cholinesterase** gene expression in mammalian cells
AUTHOR(S): **Lockridge, O.**
CORPORATE SOURCE: Univ. Michigan, Ann Arbor, MI, USA
SOURCE: Report (1990), Order No. AD-A227 610, 38 pp. Avail.: NTIS
From: Gov. Rep. Announce. Index (U. S.) 1991, 91(80, Abstr. No. 119,528
DOCUMENT TYPE: Report
LANGUAGE: English
AB A mammalian cell expression system was used to produce active human **butyrylcholinesterase** (BChE) with properties similar to the native enzyme. An addnl. advantage was the secretion of recombinant BChE into the culture medium.

L6 ANSWER 65 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:2776 HCAPLUS
DOCUMENT NUMBER: 116:2776
TITLE: Use of the polymerase chain reaction for homology probing of **butyrylcholinesterase** from several vertebrates
AUTHOR(S): Arpagaus, Martine; Chatonnet, Arnaud; Masson, Patrick; Newton, Michael; Vaughan, Theresa A.; Bartels, Cynthia F.; Nogueira, Christine P.; La Du, Bert N.; **Lockridge, Oksana**
CORPORATE SOURCE: Dep. Pharmacol., Univ. Michigan, Ann Arbor, MI, 48109-0626, USA
SOURCE: Journal of Biological Chemistry (1991), 266(11), 6966-74

CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Genomic blots from man, monkey, cow, sheep, pig, rabbit, dog, rat, mouse, guinea pig, and chicken DNA were hybridized with probes derived from the four exons of the human **butyrylcholinesterase** (BChE) gene. The results showed that the BChE gene was present in a single copy in the genome of all these vertebrates. The polymerase chain reaction was used to amplify genomic DNA from these animals with oligonucleotides derived from the human BChE coding sequence. The amplified segment contained 423 base pairs of BChE sequence, including the active site Ser-198 of the enzyme and a component of the anionic site, Asp-70. Amplification was successful for monkey, pig, cow, dog, sheep, and rabbit DNA, but unsuccessful for rat, guinea pig, mouse, and chicken DNA. Amplified segments were cloned in phage M13 and sequenced. The mouse sequence was obtained by sequencing a genomic clone. The highest identity of the human amino acid sequence was found with monkey (100%) and the lowest with mouse (91.5%). The sequence around active site Ser-198, Phe-Gly-Glu-Ser-Ala-Gly-Ala, was conserved in all 8 animals as was the anionic site component, Asp-70. A phylogenetic tree of mammalian BChEs was constructed using the partial BChE sequences.

L6 ANSWER 66 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:625268 HCAPLUS
DOCUMENT NUMBER: 115:225268
TITLE: The **butyrylcholinesterase** gene (BCHE) at 3q26.2 shows two RFLPs
AUTHOR(S): McAlpine, P. J.; Dixon, M.; Allderdice, P. W.; **Lockridge, O.**; La Du, B. N.
CORPORATE SOURCE: Dep. Hum. Genet., Univ. Manitoba, Winnipeg, MB, R3E 0W3, Can.
SOURCE: Nucleic Acids Research (1991), 19(18), 5088
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Butyrylcholinesterase** gene probes for exon 1 has a 0.8 kb PstI-HindIII insert and exon 3 has a 1.7 kb EcoRI-XbaI insert (M. Arpagaus et al., 1990). The exon 1 probe identifies two alleles on PstI digests at 23.1 kb (C1) and 4.4 kb (C2). The exon 3 probe identifies two alleles on MspI digests at 10.5 kb (D1) and 5.4 kb (D2). To date complete correspondence in phenotypes with both enzyme-probe combinations was found. Codominant inheritance was demonstrated in several two and three generation families.

L6 ANSWER 67 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:241574 HCAPLUS
DOCUMENT NUMBER: 114:241574
TITLE: Phenotypic and molecular biological analysis of human **butyrylcholinesterase** variants
AUTHOR(S): La Du, B. N.; Bartels, C. F.; Nogueira, C. P.; Hajra, A.; Lightstone, H.; Van der Spek, A.; **Lockridge, O.**
CORPORATE SOURCE: Med. Sch., Univ. Michigan, Ann Arbor, MI, 48109, USA
SOURCE: Clinical Biochemistry (1990), 23(5), 423-31
CODEN: CLBIAS; ISSN: 0009-9120
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Several variant forms of human **butyrylcholinesterase**, assocd. with unusual sensitivity to succinylcholine, are caused by specific mutations within the structural DNA coding for this enzyme. Atypical

(dibucaine-resistant) **butyrylcholinesterase** is caused by a point mutation in nucleotide position 209 (GAT-->GGT), which changes aspartate 70 to glycine. One fluoride-resistant variant family has a point mutation at nucleotide 728(ACG-->ATG), which changes threonine 243 to methionine. Another type of fluoride-resistant variant has a point mutation at nucleotide 1169 (GGT-->GTT), which changes glycine 390 to valine. One type of silent phenotype is due to a frame-shift mutation at nucleotide position 351 (GGT-->GGAG). A polymorphic site at nucleotide position 1615 (GCA/ACA), coding for Ala/Thr, accounts for the quant. K-variant, which causes an approx. one-third redn. of activity, if Thr occupies that position at codon 539. Examples are given to illustrate the advantages of using a combination of the new DNA anal. techniques, including: the use of allele-specific probes, with the std. serum **cholinesterase** phenotyping methods. More accurate typing of patients with certain variants is now possible, pedigree anal. will be aided by the improved methodol.

L6 ANSWER 68 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:222570 HCAPLUS
DOCUMENT NUMBER: 114:222570
TITLE: Proposed nomenclature for human **butyrylcholinesterase** genetic variants identified by DNA sequencing
AUTHOR(S): La Du, Bert N.; Bartels, Cynthia F.; Nogueira, Christine P.; Arpagaus, Martine; **Lockridge, Oksana**
CORPORATE SOURCE: Med. Sch., Univ. Michigan, Ann Arbor, MI, 48109-0626, USA
SOURCE: Cellular and Molecular Neurobiology (1991), 11(1), 79-89
CODEN: CMNEDI; ISSN: 0272-4340
DOCUMENT TYPE: Journal
LANGUAGE: English
AB New information identifying nucleotide alterations of human **butyrylcholinesterase** allows the use of more specific nomenclature for the variants commonly known as atypical, fluoride, silent, and K variant. In addn. to suggesting a system of trivial names and abbreviations, a list of formal names is provided that follow the guidelines of the Committee for Human Gene Nomenclature. It is suggested that formal names be included in publications whenever possible.

L6 ANSWER 69 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:173534 HCAPLUS
DOCUMENT NUMBER: 112:173534
TITLE: Evidence for a single **butyrylcholinesterase** gene in individuals carrying the C5 plasma **cholinesterase** variant (CHE2)
AUTHOR(S): Masson, Patrick; Chatonnet, Arnaud; **Lockridge, Oksana**
CORPORATE SOURCE: Unite Biochim., Cent. Rech. Serv. Sante Armees, La Tronche, 38702, Fr.
SOURCE: FEBS Letters (1990), 262(1), 115-18
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English
AB DNA of 3 unrelated individuals carrying the human blood plasma **butyrylcholinesterase** C5 variant (CHE2) was isolated from white blood cells. Southern blot patterns of DNA restriction fragments probed with each of the 4 **butyrylcholinesterase** exons provided evidence that the prodn. of C5 is not directed by a second

butyrylcholinesterase gene. Apparently, the C5 variant is a hybrid enzyme resulting from the assocn. of **butyrylcholinesterase** subunits with a non-**cholinesterase** protein.

L6 ANSWER 70 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:31437 HCAPLUS
DOCUMENT NUMBER: 112:31437
TITLE: Structure of the gene for human **butyrylcholinesterase**. Evidence for a single copy
AUTHOR(S): Arpagaus, Martine; Kott, Matthew; Vatsis, Kostas P.; Bartels, Cynthia F.; La Du, Bert N.; **Lockridge, Oksana**
CORPORATE SOURCE: Med. Sch., Univ. Michigan, Ann Abor, MI, 48109-0626, USA
SOURCE: Biochemistry (1990), 29(1), 124-31
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Five genomic clones for human **butyrylcholinesterase** (BChE) were isolated using cDNA probes encoding the catalytic subunit of the hydrophilic tetramer. The BChE gene is .gtoreq.73 kb long and contains 4 exons. Exon 1 contains untranslated sequences and 2 potential translation initiation sites at codons -69 and -47. Exon 2 (1525 bp) contains 83% of the coding sequence for the mature protein, including the N-terminal and the active-site serine, and a third possible translation initiation site (likely functional) at codon -28. Exon 3 is 167 nucleotides long. Exon 4 (604 bp) codes for the C-terminus of the protein and the 3' untranslated region where 2 polyadenylation signals were identified. Intron 1 is 6.5 kb long, and the minimal sizes of introns 2 and 3 are each 32 kb. Southern blot anal. of total human genomic DNA is in complete agreement with the gene structure established by restriction endonuclease mapping of the genomic clones; this strongly suggests that the BChE gene is present in a single copy.

L6 ANSWER 71 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1989:419788 HCAPLUS
DOCUMENT NUMBER: 111:19788
TITLE: Comparison of **butyrylcholinesterase** and **acetylcholinesterase**
AUTHOR(S): Chatonnet, Arnaud; **Lockridge, Oksana**
CORPORATE SOURCE: Dep. Physiol. Anim., Inst. Natl. Rech. Agron., Montpellier, 34060, Fr.
SOURCE: Biochemical Journal (1989), 260(3), 625-34
CODEN: BIJOAK; ISSN: 0306-3275
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review, with 123 refs., comparing **butyrylcholinesterase** (BChE) and **acetylcholinesterase** (AChE). The high homologies of the mol. forms and the homologies of the protein sequences are compared. The distribution and regulation of AChE and BChE are discussed. Finally, comparison of the structure and base compn. of the genes gives clues to understanding the origin and evolution of AChE and BChE.

L6 ANSWER 72 OF 72 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:182773 HCAPLUS
DOCUMENT NUMBER: 108:182773
TITLE: Amino acid sequence of human **cholinesterase**
AUTHOR(S): **Lockridge, O.**
CORPORATE SOURCE: Dep. Pharmacol., Michigan Univ., Ann Arbor, MI, USA

SOURCE: Report (1986), Order No. AD-A182726, 30 pp. Avail.: NTIS
From: Gov. Rep. Announce. Index (U. S.) 1987, 87(21), Abstr. No. 749,280
DOCUMENT TYPE: Report
LANGUAGE: English

AB The complete amino acid sequence of human serum **cholinesterase** was detd. The method used was Edman degrdn. of peptides purified by HPLC. There were 574 amino acid per subunit. The active site serine was located 198 amino acids from the N terminus. The active site peptide was isolated from 3 different genetic types of human **butyrylcholinesterase**: usual, atypical, and atypical-silent. The amino acid sequence of the active site peptide was identical in all 3 genotypes. Comparison of the complete sequences of **butyrylcholinesterase** from human serum and **acetylcholinesterase** from the elec. organ of Torpedo californica showed an identity of 53.8%. These structural results will serve as the basis for cloning the gene, which in turn will provide unlimited quantities of the enzyme.